

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:14:48 ; Search time 9 Seconds  
(without alignments)  
502.864 Million cell updates/sec

Title: US-10-782-141-3

Perfect score: 3556

Sequence: 1 MNKMSYQNTNEYILDGSP.....CEGVQSLETKKIVNSLFIN 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51463 seqs, 6734788 residues

Total number of hits satisfying chosen parameters: 51463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pbp.\*
- 2: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pbp.\*
- 3: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pbp.\*
- 4: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pbp.\*
- 5: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pbp.\*
- 6: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pbp.\*
- 7: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pbp.\*
- 8: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	776.5	21.8	1210	7	US-11-058-727-4
2	776.5	21.8	1210	7	US-11-108-389-4
3	754.5	21.2	1206	7	US-11-058-727-2
4	754.5	21.2	1206	7	US-11-108-389-2
5	752	21.1	673	7	US-11-058-727-14
6	752	21.1	673	7	US-11-108-389-14
7	730	20.5	669	7	US-11-058-727-6
8	730	20.5	669	7	US-11-058-727-12
9	730	20.5	669	7	US-11-108-389-6
10	730	20.5	669	7	US-11-108-389-12
11	726	20.4	673	7	US-11-058-727-34
12	726	20.4	673	7	US-11-058-727-70
13	726	20.4	673	7	US-11-108-389-34
14	726	20.4	673	7	US-11-108-389-70
15	725	20.4	675	7	US-11-058-727-48
16	725	20.4	675	7	US-11-058-727-80
17	725	20.4	675	7	US-11-108-389-48
18	725	20.4	675	7	US-11-108-389-80
19	724.5	20.4	674	7	US-11-058-727-50
20	724.5	20.4	674	7	US-11-058-727-82
21	724.5	20.4	674	7	US-11-108-389-50
22	724.5	20.4	674	7	US-11-108-389-82
23	724	20.4	673	7	US-11-058-727-22
24	724	20.4	673	7	US-11-058-727-30
25	724	20.4	673	7	US-11-058-727-58

ALIGNMENTS

RESULT 1

US-11-058-727-4  
; Sequence 4, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Preenail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; CURRENT FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1210  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-11-058-727-4

Query Match 21.8%; Score 776.5; DB 7; Length 1210;  
Best Local Similarity 30.4%; Pred. No. 9.7e-58;  
Matches 222; Conservative 130; Mismatches 272; Indels 107; Gaps 28;

QY	6	SYQNTNEYILDGSPNN--TNMSNRYPPAKDPNIFPINLD-----ACQGRP- 49
Db	2	SPNNQNEYIIDATPSTSVSNDNSNRYPPANEPNALQNMDYKDYLKMSAGNASEYVPSPE 61
QY	50	-----WQDTHESVSDIVTIGTYLQFLLEPGIGIPVIFS-IINKLIPSSQGSVAALSICD 104
Db	62	VLVSGDDAAKAAIDIV---GKLLSGLGVPFVPSIVSLYTLQIDILWPSSGQKSOWEIFMEQ 118
QY	105	LVSIIIRKEVDESVLSDGVADFEGEMTAYQDYLYLHLEDWLTDSKNPKKLADVVKQFQARE 164
Db	119	VELINQKTAETAVARNKALSELEGLGNYYQ-LYLTALKEWKENPNSRALDVRNRFIELD 177

Sequence 64, Appl  
Sequence 66, Appl  
Sequence 68, Appl  
Sequence 90, Appl  
Sequence 22, Appl  
Sequence 30, Appl  
Sequence 58, Appl  
Sequence 64, Appl  
Sequence 66, Appl  
Sequence 68, Appl  
Sequence 90, Appl  
Sequence 46, Appl  
Sequence 76, Appl  
Sequence 44, Appl  
Sequence 76, Appl  
Sequence 8, Appl  
Sequence 26, Appl  
Sequence 8, Appl  
Sequence 26, Appl  
Sequence 42, Appl



```
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-2

Query Match      21.2%; Score 754.5; DB 7; Length 1206;
Best Local Similarity 31.4%; Pred. No. 7.1e-56;
Matches 233; Conservative 119; Mismatches 258; Indels 131; Gaps 32;

QY      6 SYQNTNEYILDGSPNN--TNMSNRYPPAKDPNIPFNL-----ACQGRP- 49
Db      2 SPNNQNEYIIDATPSTSVSNDNRYPPAFNEPTNALQNMDYKDYLKMSAGNASEYPGSPE 61
QY      50 ----WQDTWESVDIVTIGTYILOFLEPGIGIPVIFS-IINKLIPSSGQSVAALSID 104
Db      62 VLVSQDAAKAADIV---GKLLSGLGVFPVGPVLSYLTQLDILWPSGKSWEIFMEQ 118
QY      105 LVSIIRKEVDESVLSDGVADFEGETAYQDYLYLHLEDWLTDSKNPKKLADVVKQFOARE 164
Db      119 VEELINQKIAEYARNKALSELGLGNVYQ-LYLTALKEEENPNRSRALRDVNRFEILD 177
QY      165 EDFTKLAGLSRQKAEILLPTTYQOANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
Db      178 SLFTQYMP-SPRVTFNFPFLTVYAMAANLHLLLDKASIFGEWGW-----STTT 227
QY      225 CNERLKAKIK---EYTNVGVWYNGKLDQIRQAGTSAEVSWSKFNKFRREMTLAVLDIAI 281
Db      228 INNYDROMKLTAEYSDHCVKWYETGLAKLK--GTSAKQWVDYVQPREMTLAVLDVVAL 285
QY      282 PPTYDFEKYPLATSVELTREIYTDVPG---YSGGNYGWERFFSFSVEANGTRGPGVLT 337
Db      286 FPNYDTRYPMTKQALTREVYTDPLGAVNVSSIGSW-YDKAPSGVIESVIRPPHVPD 344
QY      338 WLQADIIYSHSINLQGL-YLSGWGGTR-HYEDFTKNGAFORMSGTTSN--NPRNIIFGN 393
Db      345 YITGLTVYVTSQSRSSISARVIRHWAGHQISYHRVSRGSN-LQOMYGTQNLHSTSTFDFTN 403
QY      394 TDIFKIISLARVAMO-PFVGYSIPRHLVSRABFF-----PTTLNTFLYE-VNSSGYSQTI 446
Db      404 YDIYKTLSDKADVLDDIVPGYTYIFGMEPEVEFFVMVNLNTRKTLKYNPVSKDIIASTR 463
QY      447 ESVLPGINKOLPPSRT-----NYSRLSNAACVQ---NETSRVNVFGWTHTSMKKNRI 497
```

```
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-2

Query Match      21.2%; Score 754.5; DB 7; Length 1206;
Best Local Similarity 31.4%; Pred. No. 7.1e-56;
Matches 233; Conservative 119; Mismatches 258; Indels 131; Gaps 32;

QY      6 SYQNTNEYILDGSPNN--TNMSNRYPPAKDPNIPFNL-----ACQGRP- 49
Db      2 SPNNQNEYIIDATPSTSVSNDNRYPPAFNEPTNALQNMDYKDYLKMSAGNASEYPGSPE 61
QY      50 ----WQDTWESVDIVTIGTYILOFLEPGIGIPVIFS-IINKLIPSSGQSVAALSID 104
Db      62 VLVSQDAAKAADIV---GKLLSGLGVFPVGPVLSYLTQLDILWPSGKSWEIFMEQ 118
QY      105 LVSIIRKEVDESVLSDGVADFEGETAYQDYLYLHLEDWLTDSKNPKKLADVVKQFOARE 164
Db      119 VEELINQKIAEYARNKALSELGLGNVYQ-LYLTALKEEENPNRSRALRDVNRFEILD 177
QY      165 EDFTKLAGLSRQKAEILLPTTYQOANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
Db      178 SLFTQYMP-SPRVTFNFPFLTVYAMAANLHLLLDKASIFGEWGW-----STTT 227
QY      225 CNERLKAKIK---EYTNVGVWYNGKLDQIRQAGTSAEVSWSKFNKFRREMTLAVLDIAI 281
Db      228 INNYDROMKLTAEYSDHCVKWYETGLAKLK--GTSAKQWVDYVQPREMTLAVLDVVAL 285
QY      282 PPTYDFEKYPLATSVELTREIYTDVPG---YSGGNYGWERFFSFSVEANGTRGPGVLT 337
Db      286 FPNYDTRYPMTKQALTREVYTDPLGAVNVSSIGSW-YDKAPSGVIESVIRPPHVPD 344
QY      338 WLQADIIYSHSINLQGL-YLSGWGGTR-HYEDFTKNGAFORMSGTTSN--NPRNIIFGN 393
Db      345 YITGLTVYVTSQSRSSISARVIRHWAGHQISYHRVSRGSN-LQOMYGTQNLHSTSTFDFTN 403
QY      394 TDIFKIISLARVAMO-PFVGYSIPRHLVSRABFF-----PTTLNTFLYE-VNSSGYSQTI 446
Db      404 YDIYKTLSDKADVLDDIVPGYTYIFGMEPEVEFFVMVNLNTRKTLKYNPVSKDIIASTR 463
QY      447 ESVLPGINKOLPPSRT-----NYSRLSNAACVQ---NETSRVNVFGWTHTSMKKNRI 497
Db      464 DSEL-----ELPPTSDQPNYESYHRLCHITTSIPATGNTTGLVPVFSWTHRSADLNNTI 518
QY      498 YPDKITQIPAVKAF-ALPAGTYAGGYTAGGYTGDDV-----TLPYQASLKI 546
Db      519 YSDKITQIPAVKCNWNLFPV-----VYKGFGHTGGDLLQYNRSTGSGVTL-FLARYGL 571
QY      547 RLTSAPTNNKYRLRYLAGSGPGPFVRERWSPSSVSNANFSRATCG-----YSSFDVY 600
Db      572 ALEKA--GKYRVLRYATDADIVLH-----VNDQIQMPKMTNPGEDUTSKTKYA 620
QY      601 DTLVTFNQSGVEIIQN-----LSGYHLIVDKVEFIFIDIQIEKCTKQCEGIDIC 651
Db      621 DAITTLNATDSSSLAKNGLBDPNSTLSGI-VYVDRIEYFVDETY-----666
QY      652 RCEGVQSLETKEIVNSLFIN 672
```

Db 464 DSEL-----ELPETSDDPNYESYSHRLCHITSIPATGTTGLVPVFSWTHRSADLNNTI 518  
Qy 498 YPDKITQIPAVKAF-ALPAGTGYAGGYTAGPGYTGDDVV-----TLPYQASLKI 546  
Db 519 YSDKITQIPAVKWDNFPV-----VYKPGHTGGDLLQYNRSTGSGVTL-FLARYGL 571  
Qy 547 RLTSAPTNVRLRYASGGPGPRVVERWSPSSVSNANFSRPATGG-----YSSPDYV 600  
Db 572 ALEKA---GKYRVRRLRYATDAIVLH-----VNDQAQIOMPKTMNPFCEIDTSTKPKVA 620  
Qy 601 DTLVTTFNQSGVEIIQN-----LSGVHLIVDKVEFIPIDIQIEKCTKCQEGDIC 651  
Db 621 DAITYTLNATUSSLAKNLGDEPNSTLSGI-VYVDRIEFIPVDETY-----666  
Qy 652 RCEGVQSLETKKEIVNSLFIN 672  
Db 667 --EABQDLEAAKAVNALFTN 685

## RESULT 5

US-11-058-727-14

; Sequence 14, Application US/11058727

; Publication No. US20050261483A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Rafael Herrmann

; APPLICANT: Theodore W. Kahn

; APPLICANT: Albert L. Lu

; APPLICANT: Billy Fred McCutchen

; APPLICANT: James K. Presnail

; APPLICANT: James F.H. Wong

; APPLICANT: Cao-Guo Yu

; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

; TITLE OF INVENTION: Activity

; FILE REFERENCE: 35718/287809

; CURRENT APPLICATION NUMBER: US/11/058,727

; CURRENT FILING DATE: 2005-02-15

; PRIOR APPLICATION NUMBER: 60/391,786

; PRIOR FILING DATE: 2002-06-26

; PRIOR APPLICATION NUMBER: 60/460,787

; PRIOR FILING DATE: 2003-04-04

; PRIOR APPLICATION NUMBER: 10/606,320

; PRIOR FILING DATE: 2003-06-25

; NUMBER OF SEQ ID NOS: 134

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 673

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis (truncated)

US-11-058-727-14

Query Match 21.1%; Score 752; DB 7; Length 673;  
Best Local Similarity 30.5%; Pred. No. 4.9e-56;  
Matches 212; Conservative 128; Mismatches 262; Indels 92; Gaps 27;

Qy 6 SYQNTNEYILDGSPNN--TNMSNRYPPAKDNIPINLD-----ACQGRP- 49  
Db 2 SPNNQNEYIIDATPSTSVSNDNSNRYPPAFNEPTNALQNMDYKDYLKMSAGNASEYPGSP 61  
Qy 50 ----WQDTWESVDVTIGTYLQIFLEPGIGIPVIFS-IINKLIPSSGQSVAAISICD 104  
Db 62 VLVSQDAAKAIDIV---GKLLSGLGVFPVGPVLSLYTQLDILWPSGQKQWEIFMEQ 118  
Qy 105 LVSIIRKEVDESVLSDGVADFGEMTAYQDYLYHYLEDMLTKSNPKKLADVVVKQFQARE 164  
Db 119 VEELINQKIAEYARNKALSEGLEGNQY-LYLTALEEWNKPNPNSRRLRDVRNRFEILD 177  
Qy 165 EDFTKLAGLSRQKAEILLTPYQANVHLILRLDVAVKYKKEWGLVCPPLPGSGRDT 224  
Db 178 SLFTQYMP-SFRVTNFEVFLTVYTOAANLHLLLLKQASIFGEEMGW-----STTT 227

Qy 225 CNERLKAKIK---EYTNVCVGHYNKGLDQIROAGTSAEYVSKFNKFRREMTLAVLDLIAI 281  
Db 228 INNYDROKMLTAEYSDHCVKRWYETGLAKLK--GTSAKQWQVNDYNQFRREMTLTVLDVVAL 285  
Qy 282 PFTYDFEYKPLATSEVELTREIYTDVPG-----YSGNNGYGMERPFESFNSEANGTRGPGGLVT 337  
Db 286 FPNYDTRIYPMETKAQLFREYVYDPLGAVNVSSIGSW-YDKAPSGVGISSVIRPHVFD 344  
Qy 338 WLOAQDIIYSHSINLOLG-YLSCWGGRTRYHVEDFTK--GNCAFOMSGTGN--NPRNIIFG 392  
Db 345 YITGLTVVTQSRSSISSARYIRHWAG--HQISVHRIFSDNIIKQMYGTGNQLHSTSTFDFPT 402  
Qy 393 NTFDIEKILSARYAMQ-PFVGYSIPRHLVSRAREFFPTTLTFLYEVNSS-----GYQOTIE 447  
Db 403 NYDIIYKTLSKDAVLDDIVFPGYTIFFGMPVEFF-----MVNQLNNTKTLKYNPVSK 456  
Qy 448 SVLPGINK---DLPPSRT-----NYSHRLSNAACVQ-----NETSRVNVFQWTHTSKKDN 495  
Db 457 DIIAGTRDSELELPETSDQPNYESYSHRLCHITSIPATGSTTGLVPVFSWTHRSADLIN 516  
Qy 496 RIYPDKITQIPAVKAPAL-PAGTYAGGYTAGPGYTGDDVVTLVPYQASL--KIRLTSAP 552  
Db 517 AVHSDKITQIPVVKVSDLAPSIITGPNNTVVGSGPGTGGIIVKIRNGVVIISHMRVKISD 576  
Qy 553 TNKNYRVRRLRYASGGPGPRVVERWSPS-----SVSNANFSRPATGYSYSDFYVD----- 601  
Db 577 INKEYSMRIRYASANNTEFYI---NPSEENVVSHAQKTMNREALTYNKFNATLPPIKF 633  
Qy 602 TLVTTFNQSGVEIIQNLSGVHLIVDKVEFIPID 635  
Db 634 TTTEPFITLGAIFEAEDFLGIEAYIDRIEFIPVD 667

## RESULT 6

US-11-108-389-14

; Sequence 14, Application US/11108389

; Publication No. US20050261188A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Rafael Herrmann

; APPLICANT: Theodore W. Kahn

; APPLICANT: Albert L. Lu

; APPLICANT: Billy Fred McCutchen

; APPLICANT: James K. Presnail

; APPLICANT: James F.H. Wong

; APPLICANT: Cao-Guo Yu

; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

; TITLE OF INVENTION: Activity

; FILE REFERENCE: 35718/291049

; CURRENT APPLICATION NUMBER: US/11/108,389

; CURRENT FILING DATE: 2005-04-18

; PRIOR APPLICATION NUMBER: 60/391,786

; PRIOR FILING DATE: 2002-06-26

; PRIOR APPLICATION NUMBER: 60/460,787

; PRIOR FILING DATE: 2003-04-04

; PRIOR APPLICATION NUMBER: 10/606,320

; PRIOR FILING DATE: 2003-06-25

; NUMBER OF SEQ ID NOS: 134

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 673

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis (truncated)

US-11-108-389-14

Query Match 21.1%; Score 752; DB 7; Length 673;  
Best Local Similarity 30.5%; Pred. No. 4.9e-56;  
Matches 212; Conservative 128; Mismatches 262; Indels 92; Gaps 27;  
Qy 6 SYQNTNEYILDGSPNN--TNMSNRYPPAKDNIPINLD-----ACQGRP- 49  
Db 2 SPNNQNEYIIDATPSTSVSNDNSNRYPPAFNEPTNALQNMDYKDYLKMSAGNASEYPGSP 61

```

QY 50 -----WQDTWESVDIVTIGTYLIQFLLEPGIGIPVIFS-IINKLIPSSGQSVAALSICD 104
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VLVSGQDAAKAIDIV---GKLLSGLGVFPVPIVSLYQLDILWPSGQKQWEIFMEQ 118
QY 105 LVSIIRKEVDESVLSDGVADFEGETAYQDYLYLHLEDWLTDKSNPKKLADVVKQFQARE 164
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 VEELINQKIAEYARNKALSEGLGNYYQ-LYLTALAEWKENPNGRSALRDVRNRFELD 177
QY 165 EDFTKLLAGSLSRQKAEIILLPTTYQOANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
178 SLFTQVMP-SFRVTNFEVFLTYTQOANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 227
QY 225 CNERLKAKIK---EYTNVCGWYNKGLDQIRAGTSAEVWSKFNKFRREMTLAVLDIAI 281
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
228 INNYDROMKLTAEYSDHCVKMYETGLAKL-K-GTSAKQWVDYQFRRMTLAVLDVVAL 285
QY 282 PFTYFEKYPLATSVELTREIYTDVPG-----YSGNGYHWRFFSFSNVEANGTRGPGGLVT 337
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
286 FPNYDTRTPMETKAQLTREVTYDPLGAVNVSSIGSW-YDKAPSGFVIESSVIRPPHVPD 344
QY 338 WLQADIDYSHSINLQIG-YLSGWSGTRHYEDFTK--GNGAFORMSGTTSN--NPRNIIFG 392
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
345 YITGLTVYQKSISSARYIRHWAG--HQISYHRIFSDNIQKMYGTNQNLHSTSTFDFT 402
QY 393 NTDFIKIISLARYAQ-PFVGYSIPRHLVSRAEFFPTLTNTFLYEVNSS---GYSQTIE 447
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
403 NYDIYKTLSDKAVLDIVPGYTYIFFGMPEVEFF-----MVNQLNTRKTLKYNPVSK 456
QY 448 SVLPGINK---DLPPSRT-----NYSHRLSNAACVQ---NETSRVNVFGWTHSMKKDN 495
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
457 DIIAGTRDSELELPETSDQPNYESYSHRLCHITSPATGTTGLVPVFSWTHRSADLIN 516
QY 486 RIYPDKITQIPAVKAFAL-PAGTGYAGGYVTAGYTGDDVTLTPYQASL---KIRLTSAP 552
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
517 AVHSDKITQIPVVKVSDLAPSTGPNNTVWSGPGFTGGGIKVRNGVILISHMRVKISD 576
QY 553 TNKNVRLVRYASGGPGPRVERWPS-----SVSNANFSRATGGYSSFDVVD----- 601
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
577 INKYSMRIRASANTFEYI---NPSEENVKSHAKTNWNGREALTYNKNFNTATLPPIKF 633
QY 602 TLVTTFNQSGVEIIIIQNLSGVHLIVDKVEFIPID 635
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
634 TTTEPFIITLGAIFEAEDFLGIEAYIDRIEFIPVD 667

```

## RESULT 7

```

US-11-058-727-6
; Sequence 6, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 6
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Maize optimized Cry12B-1
US-11-058-727-6

```

Query Match 20.5%; Score 730; DB 7; Length 669;

Best Local Similarity 31.7%; Pred. No. 3.5e-54; Indels 116; Gaps 31;

Matches 223; Conservative 117; Mismatches 248;

```

QY 6 SYQNTNEYILDGSPNN--TNMSNRYPFKADPNIFPILND-----ACQGRP- 49
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 SPNNQNEYEIIDATPSTSVSNDNRYPFANEPNTALQNMDDYKDYKMSAGNASVPSPSE 61
QY 50 ----WQDTWESVDIVTIGTYLIQFLLEPGIGIPVIFS-IINKLIPSSGQSVAALSICD 104
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VLVSGQDAAKAIDIV---GKLLSGLGVFPVPIVSLYQLDILWPSGQKQWEIFMEQ 118
QY 105 LVSIIRKEVDESVLSDGVADFEGETAYQDYLYLHLEDWLTDKSNPKKLADVVKQFQARE 164
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 VEELINQKIAEYARNKALSEGLGNYYQ-LYLTALAEWKENPNGRSALRDVRNRFELD 177
QY 165 EDFTKLLAGSLSRQKAEIILLPTTYQOANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
178 SLFTQVMP-SFRVTNFEVFLTYTQOANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 227
QY 225 CNERLKAKIK---EYTNVCGWYNKGLDQIRAGTSAEVWSKFNKFRREMTLAVLDIAI 281
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
228 INNYDROMKLTAEYSDHCVKMYETGLAKL-K-GTSAKQWVDYQFRRMTLAVLDVVAL 285
QY 282 PFTYFEKYPLATSVELTREIYTDVPG-----YSGNGYHWRFFSFSNVEANGTRGPGGLVT 337
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
286 FPNYDTRTPMETKAQLTREVTYDPLGAVNVSSIGSW-YDKAPSGFVIESSVIRPPHVPD 344
QY 338 WLQADIDYSHSINLQIG-YLSGWSGTRHYEDFTKNGAFORMSGTTSN--NPRNIIFG 393
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
345 YITGLTVYQKSISSARYIRHWAG--HQISYHRIFSDNIQKMYGTNQNLHSTSTFDFTN 403
QY 394 TDIFIKIISLARYAQ-PFVGYSIPRHLVSRAEFF-----PTTLNTFLYE-VNSSGYSQTI 446
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
404 YDIYKTLSDKAVLDIVPGYTYIFFGMPEVEFFMVNQLNTRKTLKYNPVSKDIIASTR 463
QY 447 ESVLPGINKDLPPSRT-----NYSHRLSNAACVQ---NETSRVNVFGWTHSMKKDNRI 497
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
464 DSEL-----ELPETSQPNYESYSHRLCHITSPATGTTGLVPVFSWTHRSADLNNTI 518
QY 498 YPDKITQIPAVKAFAL-PAGTGYAGGYVTAGYTGDDVTLTPYQASLKI 546
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
519 YSDKITQIPAVKQWDLNLPVP-----VVKGPQHTGGDLLQYNRSTGSGVGL-FLARYGL 571
QY 547 RLTSAPTNNKVRVRLRYASGGPGPRVERWPSVSNANFSRATGG-----YSSFDYV 600
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
572 ALEKA---GKYRVLRYATDADIVLH-----VNDQIQOMPKTNWPGEDLSKTPKVA 620
QY 601 DTLVTTFNQSGVEIIIIQNLSGVHLIVDKVEFIPID 635
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
621 DAITTLNLATDSSLAKHNLGDPNLTSLGI-VYVDRIEFIPVD 663

```

## RESULT 8

```

US-11-058-727-12
; Sequence 12, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail

```

```
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 669
TYPE: PRT
ORGANISM: Bacillus thuringiensis (truncated)
US-11-058-727-12

Query Match      20.5%; Score 730; DB 7; Length 669;
Best Local Similarity 31.7%; Pred. No. 3.5e-54;
Matches 223; Conservative 117; Mismatches 248; Indels 116; Gaps 31;

QY      6 SYONTNEYEILDGSPNN--TMSNRYPPAKDNPINFLD-----ACQGRP- 49
Db      2 SPNNQNEYEIIDATSTSVNSDNRYPFANETNALQNDYKDYKMSAGNASSEYFGSPE 61
QY      50 ----WQDTWESVSDIVTIGTYLIQFLLEPGIGIPVIFS-IINKLIPSSGQSVAAALSICD 104
Db      62 VLVSGQDAKAIDIV---GKLSGLGVFPVGPVLSLTQTLIDILWPSEKQWEIFMEQ 118
QY      105 LVSIIRKEVDESVDGADPEGEMTAYQDYVYLHYLEDWLTDKSNPKKLADVVKQFQARE 164
Db      119 VEELINQKIAEYARNKALSEGLEGNQYQ-LYLTALEEWEENPNGRALRDVNRFEILD 177
QY      165 EDFTKLLAGSLRQKAEILLPTTYQAAVNHLLLRDAVKYKKEWGLVCPPLPGSGRTD 224
Db      178 SLFTQYMP-SFRVTNFEVDFLTYYAANAHLHLLKDSIFGEENW-----STTT 227
QY      225 CNERLKAKIK---EYTNVGVNKGDLQIRQAGTSAEYVSKFNKFRREMTLAVLDIAT 281
Db      228 INNYDRQKLTAEYSDHCWKYETGLAKLK--GTSAKQWVDYQFRREMTLAVLDVVAL 285
QY      282 PFTYDFEYKPLATSVELTREIYTDVPG-----YSGNGYGWEPFNSVEANGTRGPGLV 337
Db      286 FPNYDTRIYPMETKQALTRREVYTDPLGAVNVSSIGSW-YDKAPSGVIESSVIRPPHVD 344
QY      338 WLQADIIYSHSINLQGL-YLSGWGGTR-HYEDFTKNGAFQMSGTTN--NPRNIIFGN 393
Db      345 YITGLTVYQSRISISSARIYRWAGHQISYHVRSGSN-LQMYGTNQNLHSTSTFDFTN 403
QY      394 TDFIKIISLARVAMQ-PFVGYSIPRHLVSRAEFF-----PTLNTFLYE-VNSSGYSQTI 446
Db      404 YDIYKTLSDKADVLLDIVPGYTYIPFGMEVEFFVMVNLNTRKTLKYNPVSKDIIASTR 463
QY      447 ESVLPKINKDLPSPRT-----NYSHRLSNAACVQ---NETSRVNVFGWTHTSKDKNRI 497
Db      464 DSEL-----ELPPEISDQPNYESHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTI 518
QY      498 YPDKITQIPAVKAF-ALPAGTGYAGGYTAGPGYTGDDVV-----TLIPYQASLKI 546
Db      519 YSDKITQIPAVKCDNLPPV-----VVKPGHGTGDDLQYNRSVSGVTGL-FLARYGL 571
QY      547 RLTSAPTQKYNVRLRYAGSGPGPVERWSSVSNANFSRPAATG-----YSSFDV 600
Db      572 ALEKA---GKYRVLRYATDADIVLH-----VNDAQIQPKTNPCGEDLTSTKFKVA 620
QY      601 DFLVTFNQSGVEIIQN-----LSGYHLIVDKVEFIPID 635
Db      621 DAITTLNLTADSSALKNLGDPNSTLSGI-VYVDRIEFIPVD 663
```

```
RESULT 9
US-11-108-389-6
Sequence 6, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 669
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Maize optimized Cry1218-1
US-11-108-389-6
```

```
Query Match      20.5%; Score 730; DB 7; Length 669;
Best Local Similarity 31.7%; Pred. No. 3.5e-54;
Matches 223; Conservative 117; Mismatches 248; Indels 116; Gaps 31;

QY      6 SYONTNEYEILDGSPNN--TMSNRYPPAKDNPINFLD-----ACQGRP- 49
Db      2 SPNNQNEYEIIDATSTSVNSDNRYPFANETNALQNDYKDYKMSAGNASSEYFGSPE 61
QY      50 ----WQDTWESVSDIVTIGTYLIQFLLEPGIGIPVIFS-IINKLIPSSGQSVAAALSICD 104
Db      62 VLVSGQDAKAIDIV---GKLSGLGVFPVGPVLSLTQTLIDILWPSEKQWEIFMEQ 118
QY      105 LVSIIRKEVDESVDGADPEGEMTAYQDYVYLHYLEDWLTDKSNPKKLADVVKQFQARE 164
Db      119 VEELINQKIAEYARNKALSEGLEGNQYQ-LYLTALEEWEENPNGRALRDVNRFEILD 177
QY      165 EDFTKLLAGSLRQKAEILLPTTYQAAVNHLLLRDAVKYKKEWGLVCPPLPGSGRTD 224
Db      178 SLFTQYMP-SFRVTNFEVDFLTYYAANAHLHLLKDSIFGEENW-----STTT 227
QY      225 CNERLKAKIK---EYTNVGVNKGDLQIRQAGTSAEYVSKFNKFRREMTLAVLDIAT 281
Db      228 INNYDRQKLTAEYSDHCWKYETGLAKLK--GTSAKQWVDYQFRREMTLAVLDVVAL 285
QY      282 PFTYDFEYKPLATSVELTREIYTDVPG-----YSGNGYGWEPFNSVEANGTRGPGLV 337
Db      286 FPNYDTRIYPMETKQALTRREVYTDPLGAVNVSSIGSW-YDKAPSGVIESSVIRPPHVD 344
QY      338 WLQADIIYSHSINLQGL-YLSGWGGTR-HYEDFTKNGAFQMSGTTN--NPRNIIFGN 393
Db      345 YITGLTVYQSRISISSARIYRWAGHQISYHVRSGSN-LQMYGTNQNLHSTSTFDFTN 403
QY      394 TDFIKIISLARVAMQ-PFVGYSIPRHLVSRAEFF-----PTLNTFLYE-VNSSGYSQTI 446
Db      404 YDIYKTLSDKADVLLDIVPGYTYIPFGMEVEFFVMVNLNTRKTLKYNPVSKDIIASTR 463
QY      447 ESVLPKINKDLPSPRT-----NYSHRLSNAACVQ---NETSRVNVFGWTHTSKDKNRI 497
```

Db 464 DSEL-----ELPETSQDPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTI 518  
Qy 498 YPDKITQIPAVKAF-ALPAGTGYAGGYVTAAGPYTGDDVV-----TLPYQASLKI 546  
Db 519 YSDKITQIPAVKCDNLFPVP-----VVKPGHTGGDLLQYNRSTGSGVTGL-FLARYGL 571  
Qy 547 RLTSAPTNNKRYRRLRYASGGPGPFVRWSPSSVSNANFSRPAATGG-----YSSFDYV 600  
Db 572 ALEKA---GKYRVLRYATDADIVLH-----VNDQIQMPKTNPGEDLTSKTFKVA 620  
Qy 601 DTLVTFNQSVEIIION-----LSGYHLIVDKVEFIPIID 635  
Db 621 DAITTLNLTADSSALKHNLGDPNSTLSGI-VYVDRIEFIPVD 663

## RESULT 10

US-11-108-389-12  
; Sequence 12, Application US/11108389  
; Publication No. US20050261188A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; FILE REFERENCE: 35718/291049  
; CURRENT APPLICATION NUMBER: US/11/108,389  
; PRIOR FILING DATE: 2005-04-18  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 669  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis (truncated)  
US-11-108-389-12

Query Match 20.5%; Score 730; DB 7; Length 669;  
Best Local Similarity 31.7%; Pred. No. 3.5e-54; Mismatches 248; Indels 116; Gaps 31;  
Matches 223; Conservative 117;  
Qy 6 SYQNTNEVEILDGSPNN--TNMSNRYPPFAKDNIPFINLD-----ACQGRP- 49  
Db 2 SPNNQNEVEIIDATSTSVSNDNSNRYPPFANEPTNALQNDYKDYLMKSNAGNASEYPGSPE 61  
Qy 50 ----WQDTWESVSDIVTIGTYLIQFLPEIGIGIPVIFS-IINKLIPSSQGSVAALSID 104  
Db 62 VLVSGQDAAKAIDIV---GKLLSGLGVFPVGPVIVSLYTLQIDLILWPSGKESQWEIFMEQ 118  
Qy 105 LVSIIRKEVDSVLSDGVADPEGEMTAQDYIHLYLEDLWLTDSKSNPKKLADVVQFQARE 164  
Db 119 VEELINOKIAEYARNKALSEGLGNQYQ-LYLTALAEWEENPNPNSRALRDVRNRFELID 177  
Qy 165 EDFTKLAGLSRQKAEIALLPTYQAAVHLLLDARVKKYKWEGLVCPPLPGSGRTD 224  
Db 178 SLFTQYMP-SFRVTNFEVFPFLTVYMAANHLHLKLDASIFGEWGW-----STTT 227  
Qy 225 CNERLKAKIK---EYTNVGVGYNKGLDQIROAGTSAEYVWSKFNKFRREMTLAVLDIAI 281  
Db 228 INNYDYRQMKLTAEYSDHCWKWYETGLAKLK--GTSAKQWVDYNGFRREMTLAVLDVVAL 285

Qy 282 FPYPDEKPYPLATSVLTRYIYTDVPG-----YGGNGYGWERRFFSNVEANGTRGPGGLVT 337  
Db 286 FPNYDRTTYPMETKAQLTREYVTDPLGAVNVSSIGSW-YDKAPSGFVIESSVIRPPHVF 344  
Qy 338 WLQADIDYSHSINLQIG-YLSGNGGTR-HYEDFTKGNCAFORMSGTTSN--NPRNIIPGN 393  
Db 345 YITGLTVYTQSRSSISSARYIRHWAGHQISYHRSVRSN-LQOMYGTNQNLHSTSTFDFTN 403  
Qy 394 TDFIKIISLARYAMQ-PFVGYSIPRHLVSRAEFF-----PTTLNTELYE-VNSSGYSOTI 446  
Db 404 YDIKYTLSDKADVLLDIVPGTYTIFPGMPVEFPMVQNLNTRKTLKYNPVSKDIIIASTR 463  
Qy 447 ESVLPGINKDLPPSRT-----NYSRLSNAACVQ----NETSRVNVFGWTHSTSMKKDNRI 497  
Db 464 DSEL-----ELPETSQDPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTI 518  
Qy 498 YPDKITQIPAVKAF-ALPAGTGYAGGYVTAAGPYTGDDVV-----TLPYQASLKI 546  
Db 519 YSDKITQIPAVKCDNLFPVP-----VVKPGHTGGDLLQYNRSTGSGVTGL-FLARYGL 571  
Qy 547 RLTSAPTNNKRYRRLRYASGGPGPFVRWSPSSVSNANFSRPAATGG-----YSSFDYV 600  
Db 572 ALEKA---GKYRVLRYATDADIVLH-----VNDQIQMPKTNPGEDLTSKTFKVA 620  
Qy 601 DTLVTFNQSVEIIION-----LSGYHLIVDKVEFIPIID 635  
Db 621 DAITTLNLTADSSALKHNLGDPNSTLSGI-VYVDRIEFIPVD 663

## RESULT 11

US-11-058-727-34  
; Sequence 34, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; PRIOR FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 673  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis (mutated)  
US-11-058-727-34

Query Match 20.4%; Score 726; DB 7; Length 673;  
Best Local Similarity 31.6%; Pred. No. 7.8e-54;  
Matches 225; Conservative 116; Mismatches 244; Indels 126; Gaps 33;  
Qy 6 SYQNTNEVEILDGSPNN--TNMSNRYPPFAKDNIPFINLD-----ACQGRP- 49  
Db 2 SPNNQNEVEIIDATSTSVSNDNSNRYPPFANEPTNALQNDYKDYLMKSNAGNASEYPGSPE 61  
Qy 50 ----WQDTWESVSDIVTIGTYLIQFLPEIGIGIPVIFS-IINKLIPSSQGSVAALSID 104  
Db 62 VLVSGQDAAKAIDIV---GKLLSGLGVFPVGPVIVSLYTLQIDLILWPSGKESQWEIFMEQ 118





```
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-34

Query Match          20.4%; Score 726; DB 7; Length 673;
Best Local Similarity 31.6%; Pred. No. 7.8e-54;
Matches 225; Conservative 116; Mismatches 244; Indels 126; Gaps 33;

QY 6 SYQNTNEYILDGSPNN--TNMSNRYPPFAKDPIFPINLD-----ACQGRP- 49
Db 2 SPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYLKMSAGNASSEYFGSP 61
QY 50 -----WQDTWESVSDIVTIGTYLIQFLLEPGIGIPVIFS-IINKLIPSSGQSVAALSICD 104
Db 62 VLVSGQDAAKAAIDIV---GKLSGLGVFPVGPVLSYLTQIDILWPSEKQWEIFMEQ 118
QY 105 LVSIIRKEVDESVLSDGVADFEGETAYQDYLYHLEDWLTDSNP-----KKLADV 157
Db 119 VEELINQKIAEYARNKALSELEGNNYQ-LYLTALAEW---EENPNGRNGSRALRDVR 174
QY 158 KQFOAREEDFTKLLAGSLRQKAEIILLPTYVQAAVHLLLRDAVKYKKEWGLVCPPLY 217
Db 175 NRFEILDSLFTQMP-SFRVTNFEVPFLTVYMAAANLHLLLDKASIFGEWGW----- 227
QY 218 PGSGRTDCNERLKAKIK---EYTNVCGWYNKGLDQIROAGTSAEVSFKNFRREMTLA 274
Db 228 ---STTTINNYDROQMKLTAEYSDHCWKYETGLAKL--GTSAKQWVDYNQFREMTLA 282
QY 275 VLDIIAIFPTDYFEKYPLATSVELTREIYTDVPG-----YSGGNYGWERFFSFSNVEANGT 330
Db 283 VLDVVALFPNYDTRTPMETKQALTRVYTDPLGAVNVSSIGSW-YDKAPSGVIESVI 341
QY 331 RGPGLVTLWQAIDYSHSINLQIG-YLSGWWGTR-HYEDFTKNGAFQRMSTGTSN--NP 386
Db 342 RPPHVFYDITGLTVYTSQSSISSARIYRWAGHQISYHRVSRGSN-LQOQMYGTQNLHST 400
QY 387 RNIIFGNTDIFKIIISLARYAQ-PFVGYSIPRHLVSRAEFF-----PTLTNTFLYE-VNS 439
Db 401 STFDFNTYDIYKTLSDKAVLLDIVPGTYIIFGMEPEVEFFMVNQLNTRKLYNPSVK 460
QY 440 SGYSOTIESVLPKINDLPPSR-----NYSHRLSNAACVQ---NETSRVNVFGWTHTS 490
Db 461 DIIASTRDEL-----ELPETSQDPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRS 515
QY 491 MKKDNRIYDPDKITQIPAVKAF-ALPAGTYAGYVGTAGPGYTGDDV-----TLP 539
Db 516 ADLNNIYSDKITQIPAVKCDNLFPVP-----VVKPGHGTGDLLOYNRSTGSGVTL- 568
QY 540 YOASLKIRLTSAPTNKYRVRURYASGGPGPFRVERWSPSSVSNANFSRATGG----- 593
Db 569 FLARYGLALEKA---GKTRVRURYATDADIVLH-----VNDAAIQMPKTNPGEDLT 617
QY 594 YSSFDYDVLVTFNQSGVEIIION-----LSGVHLIVDKVEFIPID 635
Db 618 SKTFKVAADITVNLATDSSVAVKENVGDNDPNTLSGI-VYVDRIEFIPVD 667
```

RESULT 14

```
US-11-108-389-70
; Sequence 70, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-70

Query Match          20.4%; Score 726; DB 7; Length 673;
Best Local Similarity 31.6%; Pred. No. 7.8e-54;
Matches 225; Conservative 116; Mismatches 244; Indels 126; Gaps 33;

QY 6 SYQNTNEYILDGSPNN--TNMSNRYPPFAKDPIFPINLD-----ACQGRP- 49
Db 2 SPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYLKMSAGNASSEYFGSP 61
QY 50 -----WQDTWESVSDIVTIGTYLIQFLLEPGIGIPVIFS-IINKLIPSSGQSVAALSICD 104
Db 62 VLVSGQDAAKAAIDIV---GKLSGLGVFPVGPVLSYLTQIDILWPSEKQWEIFMEQ 118
QY 105 LVSIIRKEVDESVLSDGVADFEGETAYQDYLYHLEDWLTDSNP-----KKLADV 157
Db 119 VEELINQKIAEYARNKALSELEGNNYQ-LYLTALAEW---EENPNGRNGSRALRDVR 174
QY 158 KQFOAREEDFTKLLAGSLRQKAEIILLPTYVQAAVHLLLRDAVKYKKEWGLVCPPLY 217
Db 175 NRFEILDSLFTQMP-SFRVTNFEVPFLTVYMAAANLHLLLDKASIFGEWGW----- 227
QY 218 PGSGRTDCNERLKAKIK---EYTNVCGWYNKGLDQIROAGTSAEVSFKNFRREMTLA 274
Db 228 ---STTTINNYDROQMKLTAEYSDHCWKYETGLAKL--GTSAKQWVDYNQFREMTLA 282
QY 275 VLDIIAIFPTDYFEKYPLATSVELTREIYTDVPG-----YSGGNYGWERFFSFSNVEANGT 330
Db 283 VLDVVALFPNYDTRTPMETKQALTRVYTDPLGAVNVSSIGSW-YDKAPSGVIESVI 341
QY 331 RGPGLVTLWQAIDYSHSINLQIG-YLSGWWGTR-HYEDFTKNGAFQRMSTGTSN--NP 386
Db 342 RPPHVFYDITGLTVYTSQSSISSARIYRWAGHQISYHRVSRGSN-LQOQMYGTQNLHST 400
QY 387 RNIIFGNTDIFKIIISLARYAQ-PFVGYSIPRHLVSRAEFF-----PTLTNTFLYE-VNS 439
Db 401 STFDFNTYDIYKTLSDKAVLLDIVPGTYIIFGMEPEVEFFMVNQLNTRKLYNPSVK 460
QY 440 SGYSOTIESVLPKINDLPPSR-----NYSHRLSNAACVQ---NETSRVNVFGWTHTS 490
Db 461 DIIASTRDEL-----ELPETSQDPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRS 515
QY 491 MKKDNRIYDPDKITQIPAVKAF-ALPAGTYAGYVGTAGPGYTGDDV-----TLP 539
Db 516 ADLNNIYSDKITQIPAVKCDNLFPVP-----VVKPGHGTGDLLOYNRSTGSGVTL- 568
QY 540 YOASLKIRLTSAPTNKYRVRURYASGGPGPFRVERWSPSSVSNANFSRATGG----- 593
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Db 569 FLARYGLALEKA---GKRVRLRYATDADIVLH-----VNDQAIQMPKTMNPGEDLT 617
Qy 594 YSSFDYVDTLVTTFNQSGVEIIION-----LSGYHLIVDKVEFIPID 635
Db 618 SKTFKVADAITTVNLATDSSVAVKHNGLGEDPNSTLSGI-VYVDRIEFIPVD 667

RESULT 15
US-11-058-727-48
; Sequence 48, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-48
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Query Match 20.4%; Score 725; DB 7; Length 675;
Best Local Similarity 31.6%; Pred. No. 9.5e-54;
Matches 225; Conservative 116; Mismatches 244; Indels 128; Gaps 33;

Qy 6 SYQNTNEYIILDGSPNN--TNMSNRYPPAKDPNIFPINLD-----ACQGRP- 49
Db 2 SPNNQNEYIIDATPSTSVNSDSNRYPPANEPTNALQNDYKDYLKMSAGNASEYFGSPE 61
Qy 50 ----WQDTHESVSDIVTIGTYLIQFLBPGIGGIPVPS-IINKLIPSGGQVAALSICD 104
Db 62 VLVSGQDAAKAIDIV--GKLLSLGLGVFPVGPVLSVLTQLIDILWPSEKSKWEIFMEQ 118
Qy 105 LVSIIRKEVDSVLSDGVADPEGEMTAYQDYLYHLYEDWLTDKSNP-----KCLAD 155
Db 119 VEELINQKIAEYARKAULESEGLEGNQYQ-LYLTALEEW---EENPFRSRGPNGRALRD 174
Qy 156 VVKQFQAREEDFTKLLAGSLRSQKAEIILLPTVQAAVNHLLLDRAVYKKEWGLVCP 215
Db 175 VVNREIILDSLFTQMP-SFRVTNEFVPLTVYAAANLHLLLDKASIFGEWGW----229
Qy 216 LYPGSGRTDCEERLKAKIK---EYTNVYCVGWYKGLDQIRQAGTSAEVMKPNKPRREMT 272
Db 230 -----STTTINNYDROMKLTAEYSDHCVKWYETGLAKL--GTSAKQWVDYNQFREMT 282
Qy 273 LAVLDIIALFPYDFEYKPLATSVELTREIYTDVPG-----YSGNGYGERFFSFNSVEAN 328
Db 283 LAVLDVVALFPNYDTRTPMETKAQLTREYVTDPLGAVNVSSIGSW-YDKAPSFVGVISS 341
Qy 329 GTRGPGELVTLQAIIDYSHSINLQLG-YLSGWGGTR-HYEDPTKNGCAFQMSGTTSN-- 384
Db 342 VIRPHVFDYITGLVYVYTSRSISSARIYRWAGHQISYHVRSGSN-LQQMYGTNQNLH 400
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Qy 385 NPNRIIFGNTDIFKIISLARYAMQ-PFVGYSIPIRHLVSRAEFF-----PTTLATFLYE-V 437
Db 401 STSTFDFTNYDIYKTLSDKDAVLDDIVPGYTIYFFGMPDEVEFFPMVQLNNRKLTKNPNV 460
Qy 438 NSSGYSQTIIESVLPKINKDLPESRT-----NYSHRLSNAACVQ---NETSRVNVFGWTH 488
Db 461 SKDIIASTRDSSEL-----ELPPETSQDPNYESYSHRLCHITSIPATGNTTGLVPVPSWTH 515
Qy 489 TSMKKDNRIYPDKITQIPAVKAF-ALPAGTGYAGGVYTAGPGYTGDDV-----T 537
Db 516 RSADLNNTIYSDKITQIPAVKCDNLPFVP-----VVRGPGHTGGDLLQYNRSTGSGVT 569
Qy 538 LPYQASLKIRLTSAPTNNKRYRVLRYASGPGPFPRVERWSPSSVSNANFSRPATGG--- 593
Db 570 L-FLARYGLALEKA---GKRVRLRYATDADIVLH-----VNDQAIQMPKTMNPGED 617
Qy 594 --YSSFDYVDTLVTTFNQSGVEIIION-----LSGYHLIVDKVEFIPID 635
Db 618 LTSKTFKVADAITTVNLATDSSVAVKHNGLGEDPNSTLSGI-VYVDRIEFIPVD 669
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Search completed: December 15, 2005, 10:25:40  
Job time : 11 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2005, 09:53:11 ; Search time 48 Seconds  
(without alignments)  
1157.460 Million cell updates/sec

Title: US-10-782-141-3  
Perfect score: 3556  
Sequence: 1 MKNMSYQNTNEYILDGSP.....CEGVQSLETKEIVNSLFIN 672

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/prodata/1/iaa/6 COMB.pdp: \*  
3: /cgn2\_6/prodata/1/iaa/H COMB.pdp: \*  
4: /cgn2\_6/prodata/1/iaa/ECTUS COMB.pdp: \*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pdp: \*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pdp: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	831	23.4	1242	2	US-09-001-982-12
2	831	23.4	1242	2	US-09-668-650-12
3	801.5	22.5	1156	2	US-09-001-982-10
4	801.5	22.5	1156	2	US-09-002-285-70
5	801.5	22.5	1156	2	US-09-589-477-70
6	801.5	22.5	1156	2	US-10-099-285A-70
7	801.5	22.5	1156	2	US-09-668-650-10
8	773	21.7	1157	1	US-07-876-280-30
9	773	21.7	1157	1	US-07-812-180A-2
10	773	21.7	1157	1	US-08-315-468-2
11	773	21.7	1157	2	US-07-941-650A-2
12	772.5	21.7	1229	1	US-08-100-709-4
13	772.5	21.7	1229	1	US-08-176-865-4
14	772.5	21.7	1229	1	US-08-474-038-4
15	772.5	21.7	1229	1	US-08-779-046-4
16	772.5	21.7	1229	1	US-08-881-340-4
17	770.5	21.7	802	2	US-09-661-322A-30
18	765	21.5	1167	2	US-10-089-678-1
19	754	21.2	1227	2	US-09-053-549-2
20	752.5	21.2	1149	1	US-07-915-203-2
21	752.5	21.2	1149	1	US-08-272-887-2
22	752.5	21.2	1149	1	US-08-789-449-2
23	746.5	21.0	1207	1	US-07-951-715A-7
24	746.5	21.0	1207	1	US-08-459-448A-7
25	746.5	21.0	1207	2	US-08-459-595A-7
26	746.5	21.0	1207	2	US-08-459-504B-7
27	746.5	21.0	1207	2	US-08-459-444-7

28	746.5	21.0	1207	2	US-09-053-549-8	Sequence 8, Appli
29	746.5	21.0	1207	2	US-09-547-422-7	Sequence 7, Appli
30	746.5	21.0	1207	2	US-09-988-462-7	Sequence 7, Appli
31	733	20.6	1228	2	US-09-661-322A-38	Sequence 38, Appl
32	729	20.5	1169	1	US-08-315-468-4	Sequence 4, Appli
33	725.5	20.4	710	2	US-09-661-322A-42	Sequence 42, Appli
34	723.5	20.3	1227	1	US-08-448-170-8	Sequence 8, Appli
35	723.5	20.3	1227	2	US-08-961-803-9	Sequence 9, Appli
36	721.5	20.3	1227	2	US-09-661-322A-63	Sequence 63, Appl
37	718.5	20.2	1186	2	US-09-178-252-23	Sequence 23, Appl
38	718.5	20.2	1186	2	US-09-826-660-23	Sequence 23, Appl
39	716	20.1	719	2	US-08-286-870A-8	Sequence 8, Appli
40	715.5	20.1	648	2	US-08-286-870A-4	Sequence 4, Appli
41	707	19.9	643	2	US-09-178-252-25	Sequence 25, Appl
42	707	19.9	643	2	US-09-826-660-25	Sequence 25, Appl
43	689.5	19.4	1138	1	US-07-973-320-2	Sequence 2, Appli
44	689.5	19.4	1138	1	US-07-973-320-4	Sequence 4, Appli
45	688	19.3	652	2	US-08-996-441B-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1  
US-09-001-982-12  
; Sequence 12, Application US/09001982  
; Patent No. 6204246  
; GENERAL INFORMATION:  
; APPLICANT: Bosch, Hendrick J.  
; APPLICANT: Stiekema, Willem J.  
; TITLE OF INVENTION: Hybrid Toxin  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6204246artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/001,982  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/602,737  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1242 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-001-982-12

Query Match 23.4%; Score 831; DB 2; Length 1242;

Best Local Similarity 32.1%; Pred. No. 6.7e-70;

Matches 237; Conservative 128; Mismatches 246; Indels 128; Gaps 32;

QY 9 NTNEYILDGSPNTNMSN---RYPEAKDPNIPINLDACQGRP---WQD-TWESVSDIV 61

DB 2 NQNKGLI-GASNCGASDDVAKYPLANNPYSSALNLSNCSNLSNINWIIGDAKEAV 60

QY 62 TIGTYLIQFLLEPGIGG-IPVIFSLINKLI-PSSGQSVAAALSDCLVSIIRKEVDESVL 119  
Db 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGSSGQSIDLSICDLSIIDLRVSQSVLN 120  
QY 120 DGVADEGEMTAYQDYLYLHLEDLWLTDSKNPKKLA--DVVKQFQAREEDFTKLL----- 171  
Db 121 DGIADFNGLSVLYRN-YLEALDSW---NKNPNSASAEELRTRPRADSEFDRILTRGSLT 176  
QY 172 -AGSLSRQKAEILLPTVYQAAANVHLLLRDVAKYKFKFREMILAVLDIIAIPPTDYFEKY 230  
Db 177 NGGSLARQNAQIILLPSFASAAFFHLLLRDTRIGTNWG-----LYNATPPINYQSKLV 231  
QY 231 AKIKYTYNCVGVYKGLDQIRQAGTSABVSKFNKFRREMTLAVLDIIAIPPTDYFEKY 290  
Db 232 ELIELYDYCVHWYNGFNLQRGTSATAMLEFHYRREMTLWLDIVASFSSLDITNY 291  
QY 291 PLATSVELTREIYTPGVY-----SGNYGWERFF---SFNSVEANGTRGPGVLTWLOAID 343  
Db 292 PIETDFQLSRVITDPIGFVHRSSLRGESWFSFVNANFSDLE-NAIPNPRPSWFLNNMI 350  
QY 344 IYSHSINLQGLYSG-----WGGRHYEDFTKNGAF--ORMSGTTSNNPNIIFGNTDIF 397  
Db 351 ISTGSLTLPVSPSTRARVWYGSR--DRISPANSQFTELISQHTTATQTLGRN--IF 406  
QY 398 KIISLARYAMQPFVGYSPRHLVSRABFPPTT---LNTFLYE--VNSSGYS-----QTIES 448  
Db 407 RVDSQACNLNDTTYG-----VNRAVFYHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459  
QY 449 VLPNGKNDLPPTRTNYSHLSNA-----ACVQNETSRVNVFGWTHTSMKKDNRIYD 500  
Db 460 YLPGNSDI-PTPEDYTHILSTINLTGRLQVANSRSLVWYGMTHKSLARNNTINPD 518  
QY 501 KITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVV---TLPYQASLKRLTASPTNKY 557  
Db 519 RITQIPLVKGFRWGGTS-----VITGPGFTGDIILRRNTFGDFVSLQVINS-PIQRY 572  
QY 558 RVRLRYAS-----GGPGFPRVERMSPSVSNANFSPRATGYSFDDY 600  
Db 573 RLRFYASSRDARVILVTGAAGTGVGGQSVNMPLOKMTWEGNLTSR-----TFRYT 625  
QY 601 DTLVTTFNOSGVEII-----IQNLGSHYLIIVDKVEFIPIDIQIEKTKCQFEGDIC 651  
Db 626 DFSNPFSPRANPDIIIGISQPLFGAGSSGELYIDKIEILLADATFEA-----ESD-- 677  
QY 652 RCEGVQSLETKKEIVNSLF 670  
Db 678 -----LERAQKAVNALF 689

## RESULT 2

US-09-668-650-12

Sequence 12, Application US/09668650

Patent No. 6780408

GENERAL INFORMATION:

APPLICANT: Bosch, Hendrick J.

TITLE OF INVENTION: Hybrid Toxin

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6780408artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/668, 650

FILING DATE: 22-Sep-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/001,982  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/602,737  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1242 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-668-650-12

Query Match 23.4%; Score 831; DB 2; Length 1242;

Best Local Similarity 32.1%; Pred. No. 6,7e-70;

Matches 237; Conservative 128; Mismatches 246; Indels 128; Gaps 32;

QY 9 NTNEYILDGSPNNTMSN---RYPPAKDPNIPFINDACQGRP---WOD-TWESVSDIV 61  
Db 2 NQKHGII-GASCCGASDDVAKYPLANNPYSSALNLSQSSILNWINIIGDAAKEAV 60  
QY 62 TIGTYLIQFLLEPGIGG-IPVIFSLINKLI-PSSGQSVAAALSDCLVSIIRKEVDESVL 119  
Db 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGSSGQSIDLSICDLSIIDLRVSQSVLN 120  
QY 120 DGVADEGEMTAYQDYLYLHLEDLWLTDSKNPKKLA--DVVKQFQAREEDFTKLL----- 171  
Db 121 DGIADFNGLSVLYRN-YLEALDSW---NKNPNSASAEELRTRPRADSEFDRILTRGSLT 176  
QY 172 -AGSLSRQKAEILLPTVYQAAANVHLLLRDVAKYKFKWGLVCPPLYPGSGRDCNERLK 230  
Db 177 NGGSLARQNAQIILLPSFASAAFFHLLLRDTRIGTNWG-----LYNATPPINYQSKLV 231  
QY 231 AKIKYTYNCVGVYKGLDQIRQAGTSABVSKFNKFRREMTLAVLDIIAIPPTDYFEKY 290  
Db 232 ELIELYDYCVHWYNGFNLQRGTSATAMLEFHYRREMTLWLDIVASFSSLDITNY 291  
QY 291 PLATSVELTREIYTPGVY-----SGNYGWERFF---SFNSVEANGTRGPGVLTWLOAID 343  
Db 292 PIETDFQLSRVITDPIGFVHRSSLRGESWFSFVNANFSDLE-NAIPNPRPSWFLNNMI 350  
QY 344 IYSHSINLQGLYSG-----WGGRHYEDFTKNGAF--ORMSGTTSNNPNIIFGNTDIF 397  
Db 351 ISTGSLTLPVSPSTRARVWYGSR--DRISPANSQFTELISQHTTATQTLGRN--IF 406  
QY 398 KIISLARYAMQPFVGYSPRHLVSRABFPPTT---LNTFLYE--VNSSGYS-----QTIES 448  
Db 407 RVDSQACNLNDTTYG-----VNRAVFYHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459  
QY 449 VLPNGKNDLPPTRTNYSHLSNA-----ACVQNETSRVNVFGWTHTSMKKDNRIYD 500  
Db 460 YLPGNSDI-PTPEDYTHILSTINLTGRLQVANSRSLVWYGMTHKSLARNNTINPD 518  
QY 501 KITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVV---TLPYQASLKRLTASPTNKY 557  
Db 519 RITQIPLVKGFRWGGTS-----VITGPGFTGDIILRRNTFGDFVSLQVINS-PIQRY 572  
QY 558 RVRLRYAS-----GGPGFPRVERMSPSVSNANFSPRATGYSFDDY 600  
Db 573 RLRFYASSRDARVILVTGAAGTGVGGQSVNMPLOKMTWEGNLTSR-----TFRYT 625  
QY 601 DTLVTTFNOSGVEII-----IQNLGSHYLIIVDKVEFIPIDIQIEKTKCQFEGDIC 651  
Db 626 DFSNPFSPRANPDIIIGISQPLFGAGSSGELYIDKIEILLADATFEA-----ESD-- 677  
QY 652 RCEGVQSLETKKEIVNSLF 670  
Db 678 -----LERAQKAVNALF 689

Db 626 DFNPSFRANPDIIIGISEOPLFCAGSISSELYIDKIEILLADATFEA-----ESD--- 677

QY 652 RCEGVOSLETKEIVNSLF 670  
||| : : : : :  
Db 678 -----LERAQAVNALF 689

## RESULT 3

US-09-001-982-10  
; Sequence 10, Application US/09001982  
; Patent No. 6204246

; GENERAL INFORMATION:

; APPLICANT: Bosch, Hendrick J.

; APPLICANT: Stiekema, Willem J.

; TITLE OF INVENTION: Hybrid Toxin

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6204246artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/001,982

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/602,737

; FILING DATE: 21-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-541-8587

; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-001-982-10

Query Match 22.5%; Score 801.5; DB 2; Length 1156;  
Best Local Similarity 31.2%; Pred. No. 4e-67;  
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;

QY 9 NTEVEILDGSPNNTMNS--RYPEAKDPNIPFNLACQGRP---WOD-TWESVSDIV 61

Db 2 NQNKGGII--GASCCGASDDVAKYPLANNPYSSALNNSCONSSILNWINITGDAAKEAV 60

QY 62 TIGTYLIQPLBFGIGG-IPVIFSIINKLI-PSSGQSVAAALSGICDLVSIIRKEVDESVLIS 119

Db 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGGSGQSIDSLICDLISIIDLRVSGSVLN 120

QY 120 DGVADEGEMTAYQDYLLHYLEDWLTDSKNPKLA--DVVKQFQAREEFTKLL----- 171

Db 121 DGIADFNQSVLLYRN-YLEALDSW---NKNPNASAEELRTRFRIADSEFRILTRGSLT 176

QY 172 -AGSLSRQAEILLPTTYQAAVNHLLARDVAKYKKEGLVCPPLPGSGRTDCNERLK 230

Db 177 NGGSLARQNAQILLPSPFASAFFHLLLRDLATRYGTNNG-----LYNATPTFNYQSKLV 231

QY 231 AKIKEVTNYCVGWYKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIFPTDYFEKY 290

Db 232 ELIELYTYCVHWYNGFNELRQRTSATAWLEFHYRREMTLMWLDIVASFSSLDITNY 291

QY 291 PLATVELTREIYDVPVGY-----SGNGYWERFF---SFNSVEANGTRGPGVLVTLWLAID 343  
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Db 292 PIETDFQLSRVIVTDPIGFVHRSSLRGESWFSFVNANFSDLE-NAIPNRPSPWFLNNMI 350  
||| : : : : :  
QY 344 IYSHSINLQLGYSG-----WGCTRHYEDFTKGNCAF--QRMSGTTSNNPRHIIFGNTDIF 397  
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Db 351 ISTGSLTLPVSPSTDRARVWYGR--DRISPANSQFTELISGQHTTATQITILGRN--IF 406  
||| : : : : :  
QY 398 KIISLARYAMQPFVGYSIPLHLVSRAEFPPTT---LNTFELYE--VNSSGYS-----QTIES 448  
||| : : : : :  
Db 407 RVDSQACNLNDTTYG-----VNRAVYHDAEGSORSVYEGYIRITGIDNPRVQNT 459  
||| : : : : :  
QY 449 VLFGINKDLPPSRNTNYSHRLSNA-----ACVQNETSRVNVFGWTHSTMKDNRIYPD 500  
||| : : : : :  
Db 460 YLPGNSDI-PTPEDYTHILSTTINLTGRLQVNASRRSSILVMYGTWTHKSLARNNTNPD 518  
||| : : : : :  
QY 501 KITQIPAVKAFALPAGTYAGGYVYAGPVGTGGDVTLPYQASLKIRLTSAPTN--KNYR 558  
||| : : : : :  
Db 519 RITQIPLTKVDTTRGTGVSYYN-----DPGFIGGALLQRTDHGSLGLVLRVQFPLHLRQOYR 573  
||| : : : : :  
QY 559 VRLRYASGGPGPFRVERWSPSSVSNANFSRPAT-----GCYSSFDYVDVTLVTTNQ 609  
||| : : : : :  
Db 574 IRVRYAS-----TTNIRLSVNGSEGTISQNLPSFTWRLGEDLRYGSFAIREFNTSIRPTASP 629  
||| : : : : :  
QY 610 SGVEIIIQ-NLSGYHLIVDKVEPIPIQIEKCTKCFEGDICRCEGVQSLETKKEIVNS 668  
||| : : : : :  
Db 630 DQIRLTIEPSFIRQEVYVDRIEFIPVN-----PTR-----EAKEDLEAAKAVAS 674  
||| : : : : :  
QY 669 LF 670  
||| : : : : :  
Db 675 LF 676

## RESULT 4

US-09-002-285-70

; Sequence 70, Application US/09002285

; Patent No. 6369213

; GENERAL INFORMATION:

; APPLICANT: Schnepf, H. Ernest

; APPLICANT: Wicker, Carol

; APPLICANT: Narva, Kenneth E.

; APPLICANT: Walz, Michelle

; APPLICANT: Stockhoff, Brian

; APPLICANT: Muller-Cohn, Judy

; TITLE OF INVENTION: Toxins Active Against Peets

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/002,285

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/886,615

; FILING DATE: 1-JUL-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/674,002

; FILING DATE: 1-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Sanders, Jay M.

; REGISTRATION NUMBER: 39,355

; REFERENCE/DOCKET NUMBER: MA-701C2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1156 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-002-285-70

Query Match 22.5%; Score 801.5; DB 2; Length 1156;  
Best Local Similarity 31.2%; Pred. No. 46-67;  
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;  
QY 9 NTNEYEILDGSPNNTNMSN---RYPPAKDPNIPFNLNACQGRP---WQD-TWESVSDIV 61  
DB 2 NONKHGII-GASNCGCASDDVAKYPLANNPYSSALNLSNCSNIIILNWINIIGDAAKEAV 60  
QY 62 TIGTVLIQFLLEPGIGG-IPVIFSIINKLI-PSSQGSVAALSDICLVSIIRKEVDSVLS 119  
DB 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGGSSQGISDLSICDLSIIDLRVSQSVLN 120  
QY 120 DGVADEGEMTAYQDYLYLHLEDWLTDKSNPKLA--DVVKQFOAREEDFTKLL----- 171  
DB 121 DGIADFNGLSVLLYRN-YLEALDSW---NKNPNSASAEELRTRPRIADSEFDRILTRGSLT 176  
QY 172 -AGSLSRQKAEILLPTTYQAAVHLLILDVAVKKEWGLVCPPLYPGSGRTDCNERLK 230  
DB 177 NCGSLARQNAQIILLPSFASAAFFHLLLRDTRTYGTNMG-----LYNATPFINQSKLV 231  
QY 231 AKIKEYTNYCVGWYNGKGLDQIRQAGTSAEVWSKFNKFRREMTLAVLDIIAIPPTDYPEKY 290  
DB 232 ELIELYTDYCVHWYNGFNELRQGTSAWLEFHYRREMTLWLDIVASFSLDITNY 291  
QY 291 PLATSVELTREIYTPVGY-----SGNYGWERFF---SPNSVEANGTRGPGLVTLQALD 343  
DB 292 PIETDFQLSRVITYDPIGVHRSLSRGESWFSFVRANFSOLE-NAIPNRPFSWFLNNMI 350  
QY 344 IYSHINILQGLVSG---WGTRHYEDFTKNGAF--ORMSGTTSSNNPNIIFGNTDIF 397  
DB 351 ISTGSLTLVPSTDBARWYGSR--DRISPANSQFTELISGQHTTATQTLGRN--IF 406  
QY 398 KIISLARYAMQPFVGYISIPRLHVSRAEPFPTT---LNTFLYE--VNSSGYS---QTIES 448  
DB 407 RVDSQACNLNDITYG-----VNRAVFYHDASEGSRVSVEGYIRTTGIDNPRVQNT 459  
QY 449 VLPGLNKDLPPSRRTYSHRLSNA-----ACVQNETSRVNVFGWTHTSMKKDNRIYDP 500  
DB 460 YLPGENSDI-PTPEDYTHLSTTINLTGGLRQVANSRRSSLVYMGWTHKSLARNNTINPD 518  
QY 501 KITQIPAVKAPALPAGTYAGGVYTAGCYTGDDVVTLPYQASLKRLTSAPTN--KNYR 558  
DB 519 RITQIPLTKVDRTRGVSIVN-----DPGFIGALLQRTDGHSLGLVRLVQFPHLRQQR 573  
QY 559 VRLRYASGPGPFRVERMSPSVSNANFSRPAT-----GGYSSFDYVDTLVTTFNQ 609  
DB 574 IRRVYAS---TTNIRLSVNGSFGITISQNLPTMRLGEDLRYGSPFAIREFNTSIRPTASP 629  
QY 610 SGVEIIIO-NLGSYHLIVDKVBFIPIDIOIEKTCQFEGDICRCEGVOSLETKEIVNS 668  
DB 630 DQIRLTIEPSFIRQEVYVDRIEFIPV-----PTR-----EAKEDLEAAKAVAS 674  
QY 669 LF 670  
DB 675 LF 676

RESULT 5  
US-09-589-477-70  
; Sequence 70, Application US/09589477  
; Patent No. 6570005

GENERAL INFORMATION:  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Wicker, Carol  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Walz, Michelle  
APPLICANT: Stockhoff, Brian  
TITLE OF INVENTION: Toxins Active Against Pests  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/589,477  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/886,615  
FILING DATE: 1-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/674,002  
FILING DATE: 1-JUL-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-701C1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1156 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-589-477-70

Query Match 22.5%; Score 801.5; DB 2; Length 1156;  
Best Local Similarity 31.2%; Pred. No. 46-67;  
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;  
QY 9 NTNEYEILDGSPNNTNMSN---RYPPAKDPNIPFNLNACQGRP---WQD-TWESVSDIV 61  
DB 2 NONKHGII-GASNCGCASDDVAKYPLANNPYSSALNLSNCSNIIILNWINIIGDAAKEAV 60  
QY 62 TIGTVLIQFLLEPGIGG-IPVIFSIINKLI-PSSQGSVAALSDICLVSIIRKEVDSVLS 119  
DB 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGGSSQGISDLSICDLSIIDLRVSQSVLN 120  
QY 120 DGVADEGEMTAYQDYLYLHLEDWLTDKSNPKLA--DVVKQFOAREEDFTKLL----- 171  
DB 121 DGIADFNGLSVLLYRN-YLEALDSW---NKNPNSASAEELRTRPRIADSEFDRILTRGSLT 176  
QY 172 -AGSLSRQKAEILLPTTYQAAVHLLILDVAVKKEWGLVCPPLYPGSGRTDCNERLK 230  
DB 177 NCGSLARQNAQIILLPSFASAAFFHLLLRDTRTYGTNMG-----LYNATPFINQSKLV 231  
QY 231 AKIKEYTNYCVGWYNGKGLDQIRQAGTSAEVWSKFNKFRREMTLAVLDIIAIPPTDYPEKY 290  
DB 232 ELIELYTDYCVHWYNGFNELRQGTSAWLEFHYRREMTLWLDIVASFSLDITNY 291  
QY 291 PLATSVELTREIYTPVGY-----SGNYGWERFF---SPNSVEANGTRGPGLVTLQALD 343

Db 292 PIETDFQSRVYITDPGFVHRSSLRGESWFSVNRANFSDLN-NAIPNRPSPWFLNNMI 350  
QY 344 IYSHSINLQGLYSG---WGGRHYEDFTKGNF--QRMSTGTTNNPNIIFGNTDIF 397  
Db 351 ISTGSLTLPVSPSTDRARVWYGR--DRISPANSQFTELISQHTTATQTLGRN--IF 406  
QY 398 KIISLARYAMQPFVGYSPRHLVSRAPFPTT---LNTFLYE--VNSSGYS-----QTIES 448  
Db 407 RVDSQACNLNDTTYG-----VNRAVFYHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459  
QY 449 VLPKINKDLPSPRTNYSHLSNA-----ACVQNETSRVNVFGWTHTSMKKDNRIYD 500  
Db 460 YLPGENSIDI-PTPEDYTHLSTTINLTGGLRQVASNRRSSLVNMGWTHKSLARNNTINPD 518  
QY 501 KITQIPAVKAFALPAGTGYAGGVYTAGPGVYTGDDVVTLPYQASLKIRLTSAPTN--KNYR 558  
Db 519 RITQIPLTVDTRGTGVSYN-----DPGFIGALLQRTDGHSLGVLVQFPHLRQOYR 573  
QY 559 VRLRYASGGPGPRVVERWSPSSVSNANFSRPAT-----GGYSSFDYVDTLVTTFNQ 609  
Db 574 IRVRYAS-----TTNIRLSVNGSFGTISQNLPSMTMLGEDLRYGSPFAIRENTSIRPTASP 629  
QY 610 SGVEIIHQ-NLSGYHLIVDKVFEPIPIQIEKTKCFQEGDICRCBGVQSLETKEIVNS 668  
Db 630 DQIRLTIEPSFIRQEVYVDRIEFIPVN-----PTR-----EAKEDLEAAKAVAS 674  
QY 669 LF 670  
Db 675 LF 676

## RESULT 6

US-10-099-285A-70  
; Sequence 70, Application US/10099285A  
; Patent No. 6752992

## GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

Wicker, Carol

Narva, Kenneth E.

Walz, Michelle

Stockhoff, Brian

Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,285A

FILING DATE: 02-Jul-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/002,285

FILING DATE: 31-DEC-1997

APPLICATION NUMBER: US 08/886,615

FILING DATE: 1-JUL-1997

APPLICATION NUMBER: US 08/674,002

FILING DATE: 1-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-701C2D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1156 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-10-099-285A-70

Query Match 22.5%; Score 801.5; DB 2; Length 1156;  
Best Local Similarity 31.2%; Pred. No. 4e-67;  
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;

QY 9 NITVEYILDGSPNNTWNS---RYPAKDNIPINLDACQGRP---WQD-TWESVSDIV 61  
Db 2 NQKHGII-GASNCGCASDDVAKYPLANNPYSSALNLSQNSILNWINIIGDAKEAV 60  
QY 62 TIGTYLIQFLLEPGIGG-IPVIFSIINKLI-PSGQSVAAISICDLVSIIRKEVDESVL 119  
Db 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGGSSGQSIDLSICDLSIIDLRVSQSVLN 120  
QY 120 DGVADPEGEMTAYQDYLYLHLEDWLTDKSNPKLA--DVVKQFOAREEDFTKLL----- 171  
Db 121 DGIADPNSGVLLYRN-YLEALDSW---NKNPNASAEELRTRFRIADSEDFRILTRGSLT 176  
QY 172 -AGSLSRQKAEIILLPTVYQAAANVHLLLRDAVYKKEWGLVCPPLYPGSGRTDCNRLK 230  
Db 177 NGGSLARQNAQIILLPSFASAAFFHLLLRDARTYGTNWG-----LYNATPFINYQSKLV 231  
QY 231 AKIKEYTNCVGVNKGDLQIRQAGTSAEVSXPKFRREMTLAVLDIIAIPFYDPEKY 290  
Db 232 ELIELYTDYCVHYNRGNFNLQRGTSAWLEFHYRREMTLWLDIVASFSLDITNY 291  
QY 291 PLATSVELTREIYTDVPGY-----SGGNYGWERFF---SFNSVEANGTRGPGLVTLQAI 343  
Db 292 PIETDFQSRVYITDPGFVHRSSLRGESWFSVNRANFSDLN-NAIPNRPSPWFLNNMI 350  
QY 344 IYSHSINLQGLYSG---WGGRHYEDFTKGNF--QRMSTGTTNNPNIIFGNTDIF 397  
Db 351 ISTGSLTLPVSPSTDRARVWYGR--DRISPANSQFTELISQHTTATQTLGRN--IF 406  
QY 398 KIISLARYAMQPFVGYSPRHLVSRAPFPTT---LNTFLYE--VNSSGYS-----QTIES 448  
Db 407 RVDSQACNLNDTTYG-----VNRAVFYHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459  
QY 449 VLPKINKDLPSPRTNYSHLSNA-----ACVQNETSRVNVFGWTHTSMKKDNRIYD 500  
Db 460 YLPGENSIDI-PTPEDYTHLSTTINLTGGLRQVASNRRSSLVNMGWTHKSLARNNTINPD 518  
QY 501 KITQIPAVKAFALPAGTGYAGGVYTAGPGVYTGDDVVTLPYQASLKIRLTSAPTN--KNYR 558  
Db 519 RITQIPLTVDTRGTGVSYN-----DPGFIGALLQRTDGHSLGVLVQFPHLRQOYR 573  
QY 559 VRLRYASGGPGPRVVERWSPSSVSNANFSRPAT-----GGYSSFDYVDTLVTTFNQ 609  
Db 574 IRVRYAS-----TTNIRLSVNGSFGTISQNLPSMTMLGEDLRYGSPFAIRENTSIRPTASP 629  
QY 610 SGVEIIHQ-NLSGYHLIVDKVFEPIPIQIEKTKCFQEGDICRCBGVQSLETKEIVNS 668  
Db 630 DQIRLTIEPSFIRQEVYVDRIEFIPVN-----PTR-----EAKEDLEAAKAVAS 674  
QY 669 LF 670  
Db 675 LF 676

## RESULT 7

US-09-668-650-10  
; Sequence 10, Application US/09668650  
; Patent No. 6780408

GENERAL INFORMATION:  
APPLICANT: Bosch, Hendrick J.  
TITLE OF INVENTION: Hybrid Toxin  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 678040artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/668,650  
FILING DATE: 22-Sep-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/001,982  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/602,737  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-668-650-10

Query Match 22.5%; Score 801.5; DB 2; Length 1156;  
Best Local Similarity 31.2%; Pred. No. 4e-67;  
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;

QY 9 NNEYEILDGSPNNTMNS---RYFPAKDPNFPINLACQGRP---WOD-TWESVSDIV 61  
DB 2 NQNKGII-GASNCACADVAKYPLANNPYSSALNLSQNSSILNWINIIGDAKEAV 60  
QY 62 TIGTYLIQFLPEPGIGG-IPVIFSINKLI-PSSGQSVAAISICDLVSIIRKEVDESVL 119  
DB 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGSSGSGISDLSICDLLSIIDLRVSQSVLN 120  
QY 120 DGVADPEGEMTAYQDYLYHLEDWLTDSKNPKLA--DVVKQFQAREEDFTKLL----- 171  
DB 121 DGIADFNGLSVLLYRN-YLEALDSW---NKNPNASAEELRTFRADSEFDRILRGSLT 176  
QY 172 -AGSLSRQKAEILLPTVYQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLK 230  
DB 177 NGGSLARQNAQILLPLSPASAAFFHLLLRDATRYGTNWG-----LYNATPINTYQSKLV 231  
QY 231 AKIKETNYCVGVNKGDLQIRQAGTSAEVWSKFNKFRREMTLAVLDIIAIPPTDYFEKY 290  
DB 232 ELIELYTDYCVHMYNKGFLRQGTSAWLEFHYRREMTLWLDIVASFSSLDITNY 291  
QY 291 PLATSVELTREIYTDVPGY-----SGNYGWERFF---SPNSVEANGTRGPGVLWVQLAID 343  
DB 292 PIETDFQLSRVIYTDPIGVFHRSSLRGESWFSFVRANFSDLE-NAIPNRPSPFWFLNNMI 350  
QY 344 IYSHSINLQGLVSG---WGCTRYVEDFTKNGAF--QRMSTTSNNRNIIFGNTDLF 397  
DB 351 ISTGSLTLFVSPSTDRARVWYGSR--DRISPANSQFTELISGQHTATQTILGRN--IF 406

## RESULT 8

US-07-876-280-30  
Sequence 30, Application US/07876280  
Patent No. 5262158  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel M.  
APPLICANT: Cannon, Raymond J.C.  
APPLICANT: Bagley, Angela L.  
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for  
TITLE OF INVENTION: Controlling Acarides  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/876,280  
FILING DATE: 19920430  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/S 104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1157 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
STRAIN: kumamotoensis  
INDIVIDUAL ISOLATE: PS50C



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; IMMEDIATE SOURCE:
; CLONE: E. coli NM522 (pMYC2320) NRRL B-18769
; US-07-876-280-30

Query Match          21.7%; Score 773; DB 1; Length 1157;
Best Local Similarity 30.5%; Pred. No. 2.2e-64;
Matches 224; Conservative 126; Mismatches 265; Indels 120; Gaps 31;

QY 6 SYONTNEYEILDGSPNN--TNMSNRYPPFAKDPIFPINLDACQGRPWQD-----TWESVS 58
Db 2 SPNNQNEYEIIDATPSTSVSSDSNRYPFANEPT-----DALQNMNYKDYLMKSGGENPE 55
QY 59 DIVTIGTYLIQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAAALS 102
Db 56 LFGNPETFISSSTIQTGIGVIRILGALGVFFASQIASFYSFVIGQLWPSSKVDIWEIM 115
QY 103 CDLVSIIRKEVDSVLSGDVADPEGEMTAQDYVYLYHLEWLDKSNPKKLADVVQFOA 162
Db 116 ERVEELVDQKIEKYVKDKALAEKLGKLNAL-DVYQOSLEWLENRDARTSVVSNQFIA 174
QY 163 REEDFTKLAGSLRQKAEILLPTVYQAAVHLLLRDVKYKKEGLVCPPLYPGSGR 222
Db 175 LDINFVSSIP-SPAVSGHEVLLAVYAQAVNLHLLLRDASIFGEWGT-----PGEIS 228
QY 223 TDCNERLKAKIEYTNVCGWYKNGLDQIRQAGTSABVMSKFNKFRREMTLAVLDIIAIF 282
Db 229 RFYNRQVQL-TAEYSDYCVKWKYKIGLDKLNAL-DVYQOSLEWLENRDARTSVVSNQFIA 285
QY 283 PTYDFEYKPLATSVELTREIYTPDVG-----SGNYGWERF--FSFNSVEANGTRGPGL 335
Db 286 PNVDTHMYPIETTAQUTRDVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVRPPL 345
QY 336 VTWLOAIDYSHSINLQ-----GYLSGWWG--TRHYEDFTKNGAFQRMGTSTNNPRNIIF 391
Db 346 FDLSSVEINTSRGGITLNDAYINYWSGHTLKYRRTADSTVTYTYANGRITSEKNSFAL 405
QY 392 GNTDIPFKIIS-----LARYAMQPFGVYSIPR---HLVSRAEFPPFTLTFLYEVNSS---G 441
Db 406 EDRDIFEINSTVANLANYQK---AYGVPGSWFHWKRG---TSSYAYLYSKYTHALQ 459
QY 442 YSQTIESVLPGLINKDLPSPRT-----NYSHRLSNAACVQNETSRVN-----VFGWT 487
Db 460 CTQVYES-----SDEIPLDTPVVAESYSHRLSH---ITSHSPSKNGSAVYGFVFWMT 511
QY 488 HTSMKKNRIYDKITQIIPAVKAFALPAGTGYAGGYVYTAGPGYTGDDV--TLPYQASLK 545
Db 512 HTSADLNNTIYSDKITQIIPAVKGMNL-----YLGGSVWQPGPTGGDILKRTNPSILGTF 566
QY 546 IRLTSAPTNNYRVRIRYASGGPGPFPRVERWSPSSVSNANFSRPATGG---YSSFDYVD 601
Db 567 AVTVNGSLSORVVRIRYAS--TTDPEFTLYLGDITIEKNRKNFTMDNGASLTETPKFAS 624
QY 602 TLVT-TFNGSGVEIITQN---LSGYHLIVKVEFIPIDIQIEKCTQCEGDCIRCEGVQ 657
Db 625 FITDQFRTQDKILLSMDGFSGQGVYIDRIEFIPVDETY-----EAEQ 669
QY 658 SLETKKEIVNSLFIN 672
Db 670 DLEAAKAVNALFTN 684

RESULT 9
US-07-812-180A-2
; Sequence 2, Application US/07812180A
; Patent No. 5366892
; GENERAL INFORMATION:
; APPLICANT: Focerrada, Luis R
; APPLICANT: Payne, Jewel M
; APPLICANT: Sick, August J
; TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
; TITLE OF INVENTION: Thuringiensis Isolate and a No. 5366892el Gene Encoding a
; TITLE OF INVENTION: Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 2
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roman Saliwanchik
; STREET: 2421 N.W. 41st Street, Ste A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920102
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; LIBRARY: Lambdagem (TM) - 11 LIBRARY OF LUIS
; CLONE: 50C
; US-07-812-180A-2

Query Match          21.7%; Score 773; DB 1; Length 1157;
Best Local Similarity 30.5%; Pred. No. 2.2e-64;
Matches 224; Conservative 126; Mismatches 265; Indels 120; Gaps 31;

QY 6 SYONTNEYEILDGSPNN--TNMSNRYPPFAKDPIFPINLDACQGRPWQD-----TWESVS 58
Db 2 SPNNQNEYEIIDATPSTSVSSDSNRYPFANEPT-----DALQNMNYKDYLMKSGGENPE 55
QY 59 DIVTIGTYLIQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAAALS 102
Db 56 LFGNPETFISSSTIQTGIGVIRILGALGVFFASQIASFYSFVIGQLWPSSKVDIWEIM 115
QY 103 CDLVSIIRKEVDSVLSGDVADPEGEMTAQDYVYLYHLEWLDKSNPKKLADVVQFOA 162
Db 116 ERVEELVDQKIEKYVKDKALAEKLGKLNAL-DVYQOSLEWLENRDARTSVVSNQFIA 174
QY 163 REEDFTKLAGSLRQKAEILLPTVYQAAVHLLLRDVKYKKEGLVCPPLYPGSGR 222
Db 175 LDINFVSSIP-SPAVSGHEVLLAVYAQAVNLHLLLRDASIFGEWGT-----PGEIS 228
QY 223 TDCNERLKAKIEYTNVCGWYKNGLDQIRQAGTSABVMSKFNKFRREMTLAVLDIIAIF 282
Db 229 RFYNRQVQL-TAEYSDYCVKWKYKIGLDKLNAL-DVYQOSLEWLENRDARTSVVSNQFIA 285
QY 283 PTYDFEYKPLATSVELTREIYTPDVG-----SGNYGWERF--FSFNSVEANGTRGPGL 335
Db 286 PNVDTHMYPIETTAQUTRDVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVRPPL 345
QY 336 VTWLOAIDYSHSINLQ-----GYLSGWWG--TRHYEDFTKNGAFQRMGTSTNNPRNIIF 391
Db 346 FDLSSVEINTSRGGITLNDAYINYWSGHTLKYRRTADSTVTYTYANGRITSEKNSFAL 405
QY 392 GNTDIPFKIIS-----LARYAMQPFGVYSIPR---HLVSRAEFPPFTLTFLYEVNSS---G 441
```



APPLICANT: Uyeda, Kendrick A.  
APPLICANT: Bradisch, Gregory A.  
TITLE OF INVENTION: Process for Controlling Lepidopteran Pests  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/941,650A  
FILING DATE: 19920908

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/758,020  
FILING DATE: 12-SEP-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/658,935  
FILING DATE: 21-FEB-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/642,112  
FILING DATE: 16-JAN-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
STRAIN: kumamotoensis  
INDIVIDUAL ISOLATE: PS50C  
IMMEDIATE SOURCE:  
CLONE: E. coli NM522(pMYC1638), NRRL B-18751  
US-07-941-650A-2

Query Match 21.7%; Score 773; DB 2; Length 1157;  
Best Local Similarity 30.5%; Pred. No. 2.2e-64;  
Matches 224; Conservative 126; Mismatches 265; Indels 120; Gaps 31;  
QY 6 SYQNTNEYILGSPNN--TMSNRYPPAKDPNIPINLDACQRPWD-----TWESVS 58  
DB 2 SPNNQNEYIIDTSTSVSSDSDNPPFANEPT-----DALQNMNYKDYLMKSGGENPE 55  
QY 59 DIVTIGTYLIQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAAISI 102  
DB 56 LFGNPETTISSTIQIGIVGRIIGALGVPPASQIASFYFVIGLWPSKSVDIWGEIM 115  
QY 103 CDLVSIIRKEVDSEVLSDGVADPEGETAYQDYLYHLEDWLTDSKNPKKLADVVKQFOA 162  
DB 116 ERVEELVDQIEKYKDKALAKLGLGNAL-DVYQOSLEDWLENRDARTSVVSNQFTA 174  
QY 163 REEDTKLAGSLSKQAEIILLPTVQANVHLLLRDAVKYKKEWGLVCPPLYPGSGR 222  
DB 175 LDNFVSSIP-SFAVSGHEVILLAVYAQVNLHLLLRDASIFGEWGT-----PGEIS 228  
QY 223 TDCNERLXAKIKEYTNYCVGWYKNGLDQIRQAGTSAEVWWSKFNFRRENTLAVLIIAIF 282

DB 229 RFVNRQVL-TAEYSDYCVKWKIGLDKLGK-GTTSKSLNHYHQFRRENTLVLVLVALF 285  
QY 283 PTYDFEKYPLATSVELTREIYTDVGY-----SGNGYWERP--FSFNSVEANGTRGPGL 335  
DB 286 PNYDTHMYPITTAQLTRDVTYDPIAFNIVTSTGFCNPNWSTHSGILFYEVENNVIAPPHL 345  
QY 336 VTWLQADIDYSHSINLQ---GYLSGWSG-TRHYEDFTKNGCAFQRMGSGTTSNNPRNIIF 391  
DB 346 FDLSSVEINTSRGITLNDAYINYSGHTLKVRRTADSTVYTYANTYGRITSEKNSPAL 405  
QY 392 GNTDIFKIIS---LARYAMOPFVGYISIPR---HLVSRABEFPPTLTNTFLYEVSNS---G 441  
DB 406 EDRDIFEINSTVANLANYQK---AYGVPGSWFHWKKG---TSSTTAYLYSKHTHTALQG 459  
QY 442 YSQTIESVLPKINKDLPPSRT-----NYSHRLSNAACVQNETSRVN-----VFQWT 487  
DB 460 CTQVYES-----SDEIFLDRTPVAESYSHRLSH---ITSHSFKNKSGSAYTYGSFPFVMT 511  
QY 488 HTSMKKNRIYPKITQIPAKAFALPAGTCYAGGYTAGPYTGDDVW--TLPYQASLK 545  
DB 512 HTSADLNTIYSDKITQIPAVKGM---YLGGSVVGQGGFTGGDILKRTNPSILGTF 566  
QY 546 IRLTSAPTNNRYRVRVRYASGPGPFPRVERWSPSSVSNANFSRATGG---YSSFDVVD 601  
DB 567 AVTVNGSLSQRYRVRIRYAS--TTDFEFTLYLGTIEKRNKNTMDNGASLTETFKFAS 624  
QY 602 TLVT-TFNQSGVEIION---LSGYHLIVDKVEFIPIDIQIEKTKCFEGDICKCEGVQ 657  
DB 625 FITDFQFRETQDKILLSMGDFSSGQEVYIDRIEPIVDY-----EAEQ 669  
QY 658 SLETKKEIVNSLFIN 672  
DB 670 DLEAAKAVNALFTN 684

## RESULT 12

US-08-100-709-4  
Sequence 4, Application US/08100709  
Patent No. 5322687

## GENERAL INFORMATION:

APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jany, Christine S.

APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

ADDRESSEE: Nadel

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/100,709

FILING DATE: 19930729

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Egoif, Christopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-757-1590

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-100-709-4

Query Match 21.7%; Score 772.5; DB 1; Length 1229;  
 Best Local Similarity 32.1%; Pred. No. 2.7e-64;  
 Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;

QY 11 NEYEILD--GSPNNTNMSNRYPPAKDPNIFPI-----NLDACQGRPQDWTWESVSDIV 61  
 DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCAEVNND-----PFVSA-STVQTGI 60  
 QY 62 TIGTYLIQFLPGLPGIGIPVIPS-IINKLIPSSGQSVAAALSICDLVSIIRKEYDESVLSD 120  
 DB 61 NIAGRILGVLPFAGQALASFSFLVGLWP-SGRDPWEIFLHVQLRQQTENTRNT 119  
 QY 121 GVADPEGEMTAYQDYLYHLEWLTDKSNPKLADVVKQFQAREEDFTKLLAGSLR-QK 179  
 DB 120 AIARLEGLGRGVSQ-QALETWLDNRNDARSIIILERYVALELDITTAI--PLFRIRN 176  
 QY 180 AEIILLPTVQAAVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKIK---EY 236  
 DB 177 BEVPLLMVYQAANLHLLLRDASLFGSEWGM-----ASSDVNYQEQIRYTEY 227  
 QY 237 TNYCVGWNKGLDQIRQAGTSAEVMSKFNKFERMTLAVLDIIAIPPTYDFEYPLATSV 296  
 DB 228 SNHCQVWNTGLNLR--GTNAESWLRVYQFRRDLTLGLVDLVALFPSTYDTRYPINTSA 285  
 QY 297 ELTREIYDTPVYSGNGYCW--ERFF-----SFNSVEANGTRGPGVLTWLQADIIYSHSI 349  
 DB 286 QLTREIYDTPIGRTNAPSGFASTNWNFNNAAPSFAIAEAFRPPHLLDPPEQLTIYSAS- 344  
 QY 350 NLQGLVSGWGTTRHYEDFTKNGAPQMSGT-----TSNPNRIIFGNITDIFK 398  
 DB 345 -----SRWSTQHMNVVGHRLNFRPIGGTLNTSTQGLTNTSINPVTLQTSRDVYR 397  
 QY 399 IISLARYAMQPVGVSIIPRLVSRABF-PPTTLNTFLYEVNSSGYSTQIESVLPGI--- 453  
 DB 398 TESNA-----GTNLLFTTPVNGVPWFARFNINPQN--IYERGATTYQPGV--GQLFD 449  
 QY 454 -NKDLPPSRT-----NYSHRLSNAACVQNETSRVNVFGWTHTSMKDNRIYPKITQIP 506  
 DB 450 SETELPPETTERPNYESYSHRLSHGLIIGNTLRAPVSWTHRSADRTNIGPNRITQIP 509  
 QY 507 AVKAFALPAGTGYAGGYTAGPGYGGDVVTLPLYQASL-KIRLT-SAPTNKNYRVLRYA 564  
 DB 510 LVKALNL-----HSGVTVVGPGFTGGDLRLRTNTGTGFDIIRLNINVLPSQRYRIRYA 564  
 QY 565 SGGPGPFRVERWSPSSVSNANFSRPATGG-----YSSFDYVDLTVTFFN---QSGVEIII 616  
 DB 565 STTDLQF-FTRINGTTVIGNFSRTMNGDNLEYSFRTAG-PSIPFNFLNAQSTFTLGA 622  
 QY 617 QNLSYHLIVDKVEFIPIDIOIEKTKCFEGDICEGQVQSLKKEIVNSLFP 670  
 DB 623 QSFNSQEVYIDRVFVPAEVT-----EAYDIERAQKAVNALF 661

RESULT 13

US-08-176-865-4  
 Sequence 4, Application US/08176865  
 Patent No. 5616319  
 GENERAL INFORMATION:

APPLICANT: Donovan, William P.  
 APPLICANT: Tan, Yaping  
 APPLICANT: Jan, Christine S.  
 APPLICANT: Gonzalez Jr., Jose M.  
 TITLE OF INVENTION: BACILLUS THURINGIENSIS CYTET4 AND CYTETS  
 TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

ADDRESSEE: Nadel  
 STREET: 1601 Market Street, 36th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/176,865  
 FILING DATE: 30-DEC-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/100,709  
 FILING DATE: 29-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Egoie, Christopher  
 REGISTRATION NUMBER: 27633  
 REFERENCE/DOCKET NUMBER: 7205-49  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-757-1590  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-176-865-4

Query Match 21.7%; Score 772.5; DB 1; Length 1229;  
 Best Local Similarity 32.1%; Pred. No. 2.7e-64;  
 Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;

QY 11 NEYEILD--GSPNNTNMSNRYPPAKDPNIFPI-----NLDACQGRPQDWTWESVSDIV 61  
 DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCAEVNND-----PFVSA-STVQTGI 60  
 QY 62 TIGTYLIQFLPGLPGIGIPVIPS-IINKLIPSSGQSVAAALSICDLVSIIRKEYDESVLSD 120  
 DB 61 NIAGRILGVLPFAGQALASFSFLVGLWP-SGRDPWEIFLHVQLRQQTENTRNT 119  
 QY 121 GVADPEGEMTAYQDYLYHLEWLTDKSNPKLADVVKQFQAREEDFTKLLAGSLR-QK 179  
 DB 120 AIARLEGLGRGVSQ-QALETWLDNRNDARSIIILERYVALELDITTAI--PLFRIRN 176  
 QY 180 AEIILLPTVQAAVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKIK---EY 236  
 DB 177 BEVPLLMVYQAANLHLLLRDASLFGSEWGM-----ASSDVNYQEQIRYTEY 227  
 QY 237 TNYCVGWNKGLDQIRQAGTSAEVMSKFNKFERMTLAVLDIIAIPPTYDFEYPLATSV 296  
 DB 228 SNHCQVWNTGLNLR--GTNAESWLRVYQFRRDLTLGLVDLVALFPSTYDTRYPINTSA 285  
 QY 297 ELTREIYDTPVYSGNGYCW--ERFF-----SFNSVEANGTRGPGVLTWLQADIIYSHSI 349  
 DB 286 QLTREIYDTPIGRTNAPSGFASTNWNFNNAAPSFAIAEAFRPPHLLDPPEQLTIYSAS- 344  
 QY 350 NLQGLVSGWGTTRHYEDFTKNGAPQMSGT-----TSNPNRIIFGNITDIFK 398  
 DB 345 -----SRWSTQHMNVVGHRLNFRPIGGTLNTSTQGLTNTSINPVTLQTSRDVYR 397  
 QY 399 IISLARYAMQPVGVSIIPRLVSRABF-PPTTLNTFLYEVNSSGYSTQIESVLPGI--- 453  
 DB 398 TESNA-----GTNLLFTTPVNGVPWFARFNINPQN--IYERGATTYQPGV--GQLFD 449  
 QY 454 -NKDLPPSRT-----NYSHRLSNAACVQNETSRVNVFGWTHTSMKDNRIYPKITQIP 506  
 DB 450 SETELPPETTERPNYESYSHRLSHGLIIGNTLRAPVSWTHRSADRTNIGPNRITQIP 509  
 QY 507 AVKAFALPAGTGYAGGYTAGPGYGGDVVTLPLYQASL-KIRLT-SAPTNKNYRVLRYA 564

Db 510 LKALML-----HSGVTVVGPGFTGDIURRTNTGTFGDIRLNINVLPSQRVRIRYA 564  
QY 565 SGCGPGRFRVERSPSSVSNANFRPATGG-----YSSFYVDTLVTTFN-----OSGVEIII 616  
Db 565 STTDLOF-FTRINGTVNIGNSFRTNRGDNLEYSFRTAG-FSTPFNLAQSTTLGA 622  
QY 617 QNLGSHLIVDKVEFIPIDIQIEKCTKQPEGDCRCGVQSLKKEIVNSLF 670  
Db 623 QSPSNQEVYIDRVFVPAEVT-----EAYDLERAQKAVNALF 661

RESULT 14  
US-08-474-038-4  
; Sequence 4, Application US/08474038  
; Patent No. 5679343  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,038  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/176,865  
; FILING DATE: 30-DEC-1993  
; APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-474-038-4

Query Match 21.7%; Score 772.5; DB 1; Length 1229;  
Best Local Similarity 32.1%; Pred. No. 2.7e-64;  
Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;

QY 11 NEVEILD--GSPNNTNMSNRYPPAKDPNIFPI-----NLDAQCRPMDTWESVSDIV 61  
Db 7 NENEIINALSITVSNPSTQMNLSDPARIEDSLCVAEVNID-----PFVSA-STVQTGI 60  
QY 62 TGTGYLIQFLBPGIGGIVPFS-IINKLIPSGQSAALSICDLVSIIRKEVDESVLSD 120  
Db 61 NIAGRILGLVGPFAQLASFSYFLVGLWP-SGRDPWEIFLHVQLIRQQVTENTRT 119  
QY 121 GVADFEGETATQDYLYLHYLEDWLTDKSNPKKLADVVVKQFQAREEDFTKLAGSLR-QK 179

Db 120 AIALRLEGLGRGYSYQ-QALETWLDNRDARSRSIILERYVALELDITAT--PLFIRRN 176  
QY 180 AEILLPTVYQAANVHLLLRDAVKYKKEGLVCPPLYPGSGRDTCDNERLKAKIK---EY 236  
Db 177 EEPVLLMVYAQAANVHLLLRDASLFGSEWGM-----ASSDVNQYQEIRYTRYEY 227  
QY 237 TNYCVGMYNKLQDQIROAGTSAEYVMSKFNFRREMTLAVLDIIAIFPTDYDEKYPLATSV 296  
Db 228 SNHCVQWYNTGLNNLR--GTNAESWLRYNQFRDRLTLGVLDLVALFPSYDTRTYPINTSA 285  
QY 297 ELTREIYTDVPYSGGNYGM--ERFF-----SPNSVEANGTRGGLVTLWQAIDYISHSI 349  
Db 286 QLTREIYTDPIGRTNAPSGFASTNWFNNAPSPSAIEAAIFRPPHLLDFPEQLTIYSAS- 344  
QY 350 NLQGLYLSGWMGGTRHYEDFTKGNGAFORMSGT-----TSNNPRNIIFGWTDIFK 398  
Db 345 -----SRWSTQHMYVWGHRLNFRPIGGTLNTSTOGLTNTSINPVTQFTSRDVT 397  
QY 399 IISLARYAMQPFVGYISIPRHLVSRAEF-FPTTLNTFLYEVNSSGYSTIESVLPGI---- 453  
Db 398 TESNA-----GTNIIFFTPVNGVPPWAFNFINPQN--IYERGATTVSQPVQGV--GIQLPD 449  
QY 454 -NKDLPPSRT-----NYSHRLSNAACVQNETSRVNVFGWTHSTMKDNRIYDPDKITQIP 506  
Db 450 SETELPPETTERPNYESYSHRLSHIGLIIGNTLRAPVYSWTHRSADRTNTIGPNRITQIP 509  
QY 507 AVKAFALPAGTGYAGGVYTAGPGVTGGDVTLPLVQASL-KIRLT-SAPTNNRYRVLRYA 564  
Db 510 LVRALNL-----HSGVTVVGPGFTGDIURRTNTGTFGDIRLNINVLPSQRVRIRYA 564  
QY 565 SGCGPGRFRVERSPSSVSNANFRPATGG-----YSSFYVDTLVTTFN-----OSGVEIII 616  
Db 565 STTDLOF-FTRINGTVNIGNSFRTNRGDNLEYSFRTAG-FSTPFNLAQSTTLGA 622  
QY 617 QNLGSHLIVDKVEFIPIDIQIEKCTKQPEGDCRCGVQSLKKEIVNSLF 670  
Db 623 QSPSNQEVYIDRVFVPAEVT-----EAYDLERAQKAVNALF 661

RESULT 15  
US-08-779-046-4  
; Sequence 4, Application US/08779046  
; Patent No. 5854053  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,046  
; FILING DATE: 06-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match      21.7%; Score 772.5; DB 1; Length 1229;
Best Local Similarity 32.1%; Pred. No. 2.7e-64;
Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;

QY 11 NEYEILD--GSPNNTNMSNRYPPFAKDPNIFPI-----NLDACQGRPWQDTWESVSDIV 61
DB 7 NENEINALSITPTVSNPTQNMLSPDARIEDSLCVAENVNID-----PFVSA-STVQTGI 60

QY 62 TIGTVLIQFLLEPGIGGIPVIFS-IINKLIPSSGQSVAAALSICDLVSIIRKEVDESVLSD 120
DB 61 NIAGRILGVLPVAGQLASFVSVFLVGLWP-SGRDPWEIFLEHVEQLIRQQVTENTNT 119

QY 121 GVADPEGEMTAYQDYLYLHLEDWLTDKSNPKKLADVVKQFQAREEDFTKLAGSLSR-QK 179
DB 120 AIARLEGILGRGYSYQ-QALETWLDNRNDARSRIILERYVALELDITTAI--PLFRIRN 176

QY 180 AEILLPTVQAANVHLLLDAAVKYKKEWGLVCPPLYPGSGRTDCNERLKAQK--EY 236
DB 177 EEVPLLMVYAQAANLHLLLDASLFGSEWGN-----ASSDVNQYQEQIRYTEEY 227

QY 237 TNYCVGWYKGLDIQROAGTSAEVMSKFNKFEREMTLAVLDIIAIFPTVDEKYPATSV 296
DB 228 SNHCQWYNTGLNLR--GTNAESWLYNQFARDLTGLVLDVALFPSTYDTFTYINTSA 285

QY 297 ELTREIYTDVPVYSGGNYGW--ERFF-----SFNSVEANGTRGPGLVTLWLQAIIDYSHSI 349
DB 286 QLTREIYTDPIGRTNAPSGFASTNWFNNAPSFAIEAAI PRPHLLDPPEQLTIYSAS- 344

QY 350 NLQGLYLSGWGTRHYEDFTKNGAFQMSGT-----TSNNPRNIIFGNTDIFK 398
DB 345 -----SRWSSTQHMNTWVGHRLNFRPIGGTLNTSTQGLTNNTSINPVTLOFTSRDVYR 397

QY 399 IISLARVAMQPFVYSI PRHLVSRAEF-FPTTLNTFLYEVNSSGYSQTIESVLPGI--- 453
DB 398 TESNA-----GTNILETTPVNGVPWAFNFINPON--IYERGATTYSQPYQGV--GIQLFD 449

QY 454 -NKDLPPSRT-----NYSHRLSNAACVQNETSRVNVFGWTHTSMKKDNRIYPDKITQIP 506
DB 450 SETELPPETTERPNYESYSHRLSHIGLIIGNTLRAPVYSWTHRSADRTNTIGPNRITQIP 509

QY 507 AVKAPALPAGTGYAGGYTAGCYTGGDVVTLPYQASL-KIRLT-SAPTNKMYRVLRYA 564
DB 510 LVKALNL-----HSGVTYVGGSGFTGGDILRNTGTGDIRLNINPLSQRYRIRYA 564

QY 565 SGGPGPFRVERWSPSSVANPSPRATGQ-----YSSFDVDTLVTTFN-----QSGVEIII 616
DB 565 STTDLOF-FTRINGTIVNIGNFSRTRNMGDNLEYSFRTAG-FSTPFNPLNAQSTFTIGA 622

QY 617 QNLGGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCBGVQSLETKKEIVNSLF 670
DB 623 QSGSNQEVVIDRVEFVPAEVTF-----EAEYDLERAQKAVNALF 661
```

Search completed: December 15, 2005, 10:20:21  
Job time : 51 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:11:18 ; Search time 78 Seconds  
(without alignments)

3599.760 Million cell updates/sec

Title: US-10-782-141-3

Perfect score: 3556

Sequence: 1 MKNMNSYQNTNEYEILDGSP.....CEGVQSLETKKEIVNSLFIN 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3556	100.0	672	4	US-10-782-141-3
2	3540	99.6	669	4	US-10-782-141-5
3	1872	52.6	666	4	US-10-782-141-23
4	1872	52.6	666	4	US-10-782-096-23
5	1872	52.6	666	5	US-10-781-979-25
6	1571.5	44.2	693	5	US-10-781-979-3
7	1561.5	43.9	690	5	US-10-781-979-5
8	918.5	25.8	674	4	US-10-782-141-20
9	918.5	25.8	674	4	US-10-782-096-21
10	918.5	25.8	674	4	US-10-782-570-17
11	918.5	25.8	674	5	US-10-783-417-15
12	918.5	25.8	674	5	US-10-781-979-22
13	833.5	23.4	682	4	US-10-782-096-2
14	801.5	22.5	1151	6	US-11-018-615-13
15	801.5	22.5	1156	4	US-10-099-285-70
16	801.5	22.5	1156	6	US-11-018-615-12
17	782.5	22.0	671	4	US-10-782-096-4
18	776.5	21.8	1210	4	US-10-032-717-4
19	776.5	21.8	1210	4	US-10-414-637-4
20	776.5	21.8	1210	4	US-10-606-320-4
21	776.5	21.8	1210	4	US-10-746-914-4
22	773	21.7	1157	4	US-10-782-141-16
23	773	21.7	1157	4	US-10-782-096-17
24	773	21.7	1157	4	US-10-782-570-13
25	773	21.7	1157	5	US-10-783-417-11
26	773	21.7	1157	5	US-10-781-979-18
27	773	21.7	1157	5	US-10-926-819-15

28	770.5	21.7	802	4	US-10-428-961-30	Sequence 30, Appl
29	765.5	21.5	661	4	US-10-782-096-6	Sequence 6, Appl
30	765	21.5	1167	4	US-10-089-678-1	Sequence 1, Appl
31	756.5	21.3	719	5	US-10-926-819-30	Sequence 30, Appl
32	756.5	21.3	719	5	US-10-926-819-31	Sequence 31, Appl
33	756	21.3	1228	5	US-10-926-819-8	Sequence 8, Appl
34	754.5	21.2	1206	4	US-10-032-717-2	Sequence 2, Appl
35	754.5	21.2	1206	4	US-10-414-637-2	Sequence 2, Appl
36	754.5	21.2	1206	4	US-10-606-320-2	Sequence 2, Appl
37	754.5	21.2	1206	4	US-10-746-914-2	Sequence 2, Appl
38	754	21.2	1228	4	US-10-809-953-10	Sequence 10, Appl
39	752	21.1	667	4	US-10-032-717-8	Sequence 8, Appl
40	752	21.1	667	4	US-10-414-637-8	Sequence 8, Appl
41	752	21.1	673	4	US-10-032-717-18	Sequence 18, Appl
42	752	21.1	673	4	US-10-414-637-18	Sequence 18, Appl
43	752	21.1	673	4	US-10-606-320-14	Sequence 14, Appl
44	752	21.1	673	4	US-10-746-914-14	Sequence 14, Appl
45	746.5	21.0	1207	3	US-09-988-462-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1

US-10-782-141-3

; Sequence 3, Application US/10782141

; Publication No: US20040197917A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and

; FILE OF INVENTION: Methods for Its Use

; FILE REFERENCE: 045600/274143

; CURRENT APPLICATION NUMBER: US/10/782,141

; CURRENT FILING DATE: 2004-02-20

; PRIOR APPLICATION NUMBER: 60/448,632

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 672

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

; US-10-782-141-3

Query Match 100.0%; Score 3556; DB 4; Length 672;

Best Local Similarity 100.0%; Pred. No. 5.2e-304; Mismatches 0; Indels 0; Gaps 0;

Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKNMNSYQNTNEYEILDGSPNTNMNSRYPFAKDPNIFPINLDACQRPWQDTWESVSDI 60

Db 1 MKNMNSYQNTNEYEILDGSPNTNMNSRYPFAKDPNIFPINLDACQRPWQDTWESVSDI 60

QY 61 VTIGTYLIQFLLEPGGIGPVIPIFIIINKLIPSSGQSVAAISICDLVSIIRKEVDESVLSD 120

Db 61 VTIGTYLIQFLLEPGGIGPVIPIFIIINKLIPSSGQSVAAISICDLVSIIRKEVDESVLSD 120

QY 121 GVADPEGEANTQDYVLYHYLEDWLTOKSNPKLADVVKQFAREEDFTKLLAGLSRQKA 180

Db 121 GVADPEGEANTQDYVLYHYLEDWLTOKSNPKLADVVKQFAREEDFTKLLAGLSRQKA 180

QY 181 EILLPTTYQAAVNHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLKAKIKEYTNYC 240

Db 181 EILLPTTYQAAVNHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLKAKIKEYTNYC 240

QY 241 VGMYNKGLDQIRQAGTSAEVWSKFNKFRREMTLAVLDIIAIFPTDFEKPPLATSVELTR 300

Db 241 VGMYNKGLDQIRQAGTSAEVWSKFNKFRREMTLAVLDIIAIFPTDFEKPPLATSVELTR 300

QY 301 EYTPDVGSGGNYGWERFFSVEANGTRGPGVTWLQADIIYSHSINLQLGYSWG 360

```
Db 301 EITVDVSGNYGWERFFSFNSVEANGTRGPGVLTWLAQADIIYSHSINLQGLYSGWG 360
Qy 361 GTRHYEDFTKNGAFORMSGTSSNNPRNII FGNITDIFKII SLARYAMQPFVGYSPRHLY 420
Db 361 GTRHYEDFTKNGAFORMSGTSSNNPRNII FGNITDIFKII SLARYAMQPFVGYSPRHLY 420
Qy 421 SRAEFPPTLTNTFLYEVNSSGYSTIESVLPKINLDPSPRTNYSHRLSNAACVQNETSR 480
Db 421 SRAEFPPTLTNTFLYEVNSSGYSTIESVLPKINLDPSPRTNYSHRLSNAACVQNETSR 480
Qy 481 VNVFGWHTSMKKNRIYDPDKITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVVTLPL 540
Db 481 VNVFGWHTSMKKNRIYDPDKITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVVTLPL 540
Qy 541 QASLKIRLTSAPTNNKYRVRLEYASGGPGPFVRERWSPSSVSNANFSRPAATGGYSSFDYV 600
Db 541 QASLKIRLTSAPTNNKYRVRLEYASGGPGPFVRERWSPSSVSNANFSRPAATGGYSSFDYV 600
Qy 601 DTLVTFNQSGVEIIIONLSGYHLIVDKVEFIPIDIIQIEKCTKCOPEGDICRCEGVQSLE 660
Db 601 DTLVTFNQSGVEIIIONLSGYHLIVDKVEFIPIDIIQIEKCTKCOPEGDICRCEGVQSLE 660
Qy 661 TKKEIVNSLFIN 672
Db 661 TKKEIVNSLFIN 672
```

## RESULT 2

```
US-10-782-141-5
; Sequence 5, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; CURRENT APPLICATION NUMBER: US/10782, 141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-5
```

```
Query Match 99.6%; Score 3540; DB 4; Length 669;
Best Local Similarity 100.0%; Pred. No. 1.3e-302;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MNSYQNTNEYELDGSPPNNTNMSNRYPPAKDPNIPINLDACQGRPWQDTWESVDIVTI 63
Db 1 MNSYQNTNEYELDGSPPNNTNMSNRYPPAKDPNIPINLDACQGRPWQDTWESVDIVTI 60

Qy 64 GTYLQFLLEPGIGGIPVIFSINKLIPSSGQSVAAALSICDLVSIIRKEVDESVLSDGVA 123
Db 61 GTYLQFLLEPGIGGIPVIFSINKLIPSSGQSVAAALSICDLVSIIRKEVDESVLSDGVA 120

Qy 124 DFEGMTAYQDYLYHYLEDWLTDKSNPKKLADVVKQFOAREDDFTKLLAGSLSRQAEIL 183
Db 121 DFEGMTAYQDYLYHYLEDWLTDKSNPKKLADVVKQFOAREDDFTKLLAGSLSRQAEIL 180

Qy 184 LLPTVQQAANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLKAKIKETNYVCWG 243
Db 181 LLPTVQQAANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLKAKIKETNYVCWG 240
```

```
Qy 244 YNKGLDQIRQACTSAEVMKFNKFRREMTLAVLDIIAIFPTDYDFEKYPLATSVELTREIY 303
Db 241 YNKGLDQIRQACTSAEVMKFNKFRREMTLAVLDIIAIFPTDYDFEKYPLATSVELTREIY 300

Qy 304 TDPVGYSGNYGWERFFSFNSVEANGTRGPGVLTWLAQADIIYSHSINLQGLYSGWGTR 363
Db 301 TDPVGYSGNYGWERFFSFNSVEANGTRGPGVLTWLAQADIIYSHSINLQGLYSGWGTR 360

Qy 364 HYEDFTKNGAFORMSGTSSNNPRNII FGNITDIFKII SLARYAMQPFVGYSPRHLYSRA 423
Db 361 HYEDFTKNGAFORMSGTSSNNPRNII FGNITDIFKII SLARYAMQPFVGYSPRHLYSRA 420

Qy 424 EFPPTLTNTFLYEVNSSGYSTIESVLPKINLDPSPRTNYSHRLSNAACVQNETSRVNV 483
Db 421 EFPPTLTNTFLYEVNSSGYSTIESVLPKINLDPSPRTNYSHRLSNAACVQNETSRVNV 480

Qy 484 FGWHTSMKKNRIYDPDKITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVVTLPLQAS 543
Db 481 FGWHTSMKKNRIYDPDKITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVVTLPLQAS 540

Qy 544 LKIRLTSAPTNNKYRVRLEYASGGPGPFVRERWSPSSVSNANFSRPAATGGYSSFDYDVL 603
Db 541 LKIRLTSAPTNNKYRVRLEYASGGPGPFVRERWSPSSVSNANFSRPAATGGYSSFDYDVL 600

Qy 604 VTFNQSGVEIIIONLSGYHLIVDKVEFIPIDIIQIEKCTKCOPEGDICRCEGVQSLETKK 663
Db 601 VTFNQSGVEIIIONLSGYHLIVDKVEFIPIDIIQIEKCTKCOPEGDICRCEGVQSLETKK 660

Qy 664 EIVNSLFIN 672
Db 661 EIVNSLFIN 669
```

## RESULT 3

```
US-10-782-141-23
; Sequence 23, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; CURRENT APPLICATION NUMBER: US/10782, 141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-23
```

```
Query Match 52.6%; Score 1872; DB 4; Length 666;
Best Local Similarity 57.0%; Pred. No. 1.5e-155;
Matches 392; Conservative 91; Mismatches 161; Indels 44; Gaps 15;

Qy 5 NSYQNTNEYELDGSPPNNTNMSNRYPPAKDPNIPINLDACQGRPWQDTWESVDIVTI 64
Db 1 NSYQNTNEYELDGSPPNNTNMSNRYPPAKDPNIPINLDACQGRPWQDTWESVDIVTI 60

Qy 65 TYLQFLLEPGIGGIPVIFSINKLIPSSGQSVAAALSICDLVSIIRKEVDESVLSDGVAD 124
Db 61 IDLIEFLMEPLSGGINTLPSIIIGKLIPTNHQSVSALSICDLVSIIRKEVADSVLSDAICR 120

Qy 125 F-EGEMTAYQDYLYHYLEDWLT-----KSNPKKLADVVKQFOAREDDFTKLLAGSLSRQ 178
Db 121 FLDGKLKNRYEYLPLEAWLKDGPLOKNTNNSDIOQLVKYFELSRDFNEILGGLSARN 180
```





```

Db 1 NSYENKNEYELSSNNNTNPNRYPPFANDRDMSTMSPNDCCGISWDEIWESAFTISG 60
Qy 65 TYLQFLLEPGIGIPVIFSIINKLIPSSGQSAALSICDLVSIIRKEVDESVLSDGVAD 124
Db 61 IDLIEFLMEPLSGGINTLFSIIGKLIPTNHOSVSALSICDLVSIIRKEVADSVLSDAICR 120
Qy 125 F-EGEMTAYQDYLYHLVLEDLTD-----KSNPKKLADVVKQFOAREEDFTKLGLAGSLRQ 178
Db 121 FLDGKLNRYREYLYLEAWLKDGPLOKTNNSDYGQVYKYPFELSERDFNEILGSLARN 180
Qy 179 KAEIILLPTVYQAANVHLLLRDAVYKKEW-----GLVCPPLYPGSG---RTDCNER 228
Db 181 NAQIILLPYFCASCCKQLLLLRDAVYEQWFPFLSAENVRSELSPNSGCDFTGDYER 240
Qy 229 LKAKIKEYTNYCVGYNKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIFPTDPE 288
Db 241 LKCKIAEYTDYCEVYQAGLNQIKQAGTGADTWAKFNKFRREMTLVLDDIIAIFQYDFK 300
Qy 289 KYPLATSVELTREIYTDVPGYSGGNYGWERFF--SFNSVEANGTRGPGGLVTLWLAIDYS 346
Db 301 KYPLPHTVELTREIYTDVPGYSSGTYSWLKYWTGAFNTLEANGTRGPGGLVTLWLSIGYN 360
Qy 347 HSINLQGLYSGWGTRHYEDFTKNGAFORMSGTTSNNPRNIIFGNTDIFKIIILARYA 406
Db 361 EYVS---RYFSGWGTTRHYEDYTTGNGFNGFORMSGTTSNDRDISPNSDIFKIES---KA 414
Qy 407 MOPFVG--YSTPRHIVSRAEPFPTTLNTFLYEVNSSGY-SQIESVLPGINKDLPPSRTN 463
Db 415 IMNLVGEINARPEYRVSRAEFSESTAFIYLYDAGNSGLSMTITSKLPGI-KNPEPSYRD 473
Qy 464 YSHRLSNAACVQNETSRVNVFGWTHSTSMKKNRIYDPDKITQIPAVKAFALPAGTYAGGY 523
Db 474 YSHRLSNAACVAGNSRINNVGWTHTSMKKNLIYDPDKITQIPAVKAFDI-SDTG--PGQ 530
Qy 524 VTAGPGYTGVDVTLPYQASLKIRLTSAPTNNKRYRVLRYAGGPGPFRVERWSPSSVSN 583
Db 531 VIAGPGHTGNNVSVLPYYSRLKIRLIPASTNKYLVRYRTSTNGRLLVERWSPSSIN 590
Qy 584 ANFSRPAATGSSPDYDVTLTFTFNQSGVEIIQNLGSHVHLVDKVEFIPIDIEKCTK 643
Db 591 SYFFLPSTPGDSFGYDVTLTFTFNQSGVEIIQNLGSHVHLVDKVEFIPVNV-----STA 644
Qy 644 COFEGDICRCEGVQSLTKKEIVNSLFI 671
Db 645 LEYEGK-----QSLKAQDVVNDLFV 665

```

## RESULT 6

US-10-781-979-3

; Sequence 3, Application US/10781979

; Publication No. US20040250311A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and

; FILE REFERENCE: 045600/274147

; CURRENT APPLICATION NUMBER: US/10/781,979

; PRIOR FILING DATE: 2004-02-20

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 693

; TYPE: PR1

; ORGANISM: Bacillus thuringiensis

US-10-781-979-3

Query Match 44.2%; Score 1571.5; DB 5; Length 693;  
 Best Local Similarity 47.2%; Pred No. 5.1e-129;  
 Matches 340; Conservative 107; Mismatches 198; Indels 75; Gaps 18;

```

Qy 1 MKNMNSYQNTWEYELDGSPNNTNMSNRYPPFADKNIPFINLDACQGRPWQDTWESVDI 60
Db 1 MKMNSPYQNKNEYELSSNNNTNPNRYPPFANNRDMSTMSPNDCCGISWDEIWESVETI 60
Qy 61 VTIGYLYLQFLLEPGIGIPVIFSIINKLIPSSGQSAALSICDLVSIIRKEVDESVLSD 120
Db 61 TSIGNLNLEFVLEPSLGGINTLFSIIGKLIPTNRQTVSALSICDLVSIIRKEVADSVLSD 120
Qy 121 GVADPEGEMTAYQDYLYHLVLEDLTD-----KSNPKKLADVVKQFOAREEDFTKLGLAGSL 175
Db 121 ATADFDGKLNRYREYLYLEAWLKDGPLOKTNNSDYGQVYKYPFELSERDFNEILGSL 180
Qy 176 SRQKAEIILLPTVYQAANVHLLLRDAVYKKEW-----GLVCPPLYPGSG---RTDC 225
Db 181 SRNNAQVLLPTFAQAANVHLLLRDAVYKQWPPFLSAENVRSELSPNSGCDFTGDY 240
Qy 226 NERLKAKIKEYTNYCVGYNKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIFPTT 285
Db 241 YERLCKCTAEYTNCLYQVGLNQIKQAGTGADTWKFNKFRREMTLAVLDIIAIFPTT 300
Qy 286 DPEKYPLATSVELTREIYTDVPGYSGGNYGWERFF--SFNSVEANGTRGPGGLVTLWLAID 343
Db 301 DPEKPLPHTVELTREIYTDVPGYSSGTYSWLKNWNTFNGLANGTRGPGGLVTLWLSKIG 360
Qy 344 IYSHSINLQGLYSGWGTRHYEDFTKNGAFORMSGTTSNNPRNIIFGNTDIFKIIISLA 403
Db 361 IYNEVVS---RYFAGWGTTRHYEDYTTGNGIIFORMSGTTSNDRIDFQNAVYKITSL- 416
Qy 404 RYAMPQPFVGYSI--PHRLVSRABFPPTTLNTFLYEVNSSGYQ-TIESVLP-----GIN 454
Db 417 --AIMNLVGEITTAPEYRVSRAEFSESTAFIYLYDAGNGLSMTITESTPPLVHNGVR 474
Qy 455 KDLPSRTNYSRLSNAACVQNETSRVNVFGWTHSTSMKKNRIYDPDKITQIPAVKAFALP 514
Db 475 -----GPSHRLSNAACVYGVNSRVNVYGTHTSLKRENIIEANQITQIPAVKSYLQ 526
Qy 515 AGTYAGGYVTAGPGYTGDDVTL-----PYQA-----SLKIRLTSAPTNNKRYRVLRYA 564
Db 527 NYLANAYTVVIKGT-HTGDLIRFLRTKSEYNNAVYAGGGIRLIINNKTAQGSYRIRPYA 585
Qy 565 SGGPGPFRVERWSPSSVSN--ANFSRPAATG-----YSSPDYDVTLTFTFNQSGVEIIQ 617
Db 586 ADKAAFFSYLYPGGWSNRFSVLSKYSYSGNYDDLKYSDFKFAEIIITPPLPSSNIQMDVE 645
Qy 618 N-----LSGYHLIVDKVEFIPIDIEKCTKCOFEGDICRCEGVQSLTKKEIVNSLFIN 672
Db 646 MOANSFQSDVNVVLDKIEFLP-----SNTTTLEYEGE-----RDLKTKNAVNDLFTN 693

```

## RESULT 7

US-10-781-979-5

; Sequence 5, Application US/10781979

; Publication No. US20040250311A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and

; FILE REFERENCE: 045600/274147

; CURRENT APPLICATION NUMBER: US/10/781,979

; PRIOR FILING DATE: 2004-02-20

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

```
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-5

Query Match      43.9%; Score 1561.5; DB 5; Length 690;
Best Local Similarity 47.1%; Pred. No. 3.8e-128;
Matches 338; Conservative 107; Mismatches 197; Indels 75; Gaps 18;

QY 4 MNSYQNTNEVEILLDGSNNNTMSNRYPPFAKDPNIPINLDACQGRPWQDTWESVIVTI 63
Db 1 MSYQNKNEVEILLSSNNNTNTPRPFANNRDMSTWMDCCGIGWDEIWEVETISI 60

QY 64 GTYLIOFLLEPGIGGIPVFSIINKLIPSGQVAALSICDLVSIIRKEVDESGLSDGVA 123
Db 61 GINLIEFVLEPSLGGINTLLSIIGKLPNTQVTSALSICDLVSIIRKEVADSVLSDAIA 120

QY 124 DFEGETAYQDYLYLHLEWLT-----XSNPKKLADVVKQFQARBEDFTKLALAGLSRQ 178
Db 121 DFDGKLKNRYEYLYSLGAWLKDGKPLQKTNNSDIGOLVYYPKLSERDFNEILGGSLRN 180

QY 179 KAEILLPTVQAAVHLLLRDAVKKYKKEW-----GLVCPPLYPGSG---RTDCNR 228
Db 181 NAOVLLPTFAQAAVQVLLLRDAVQYKQWPFPLSAENVRSLSIPNSGCDFTGDYER 240

QY 229 LKAKIKEYTNYCVGWYKGLDQIROAGTSAEVMKSKENKFRREMTLAVLDIIAIFPTVDPE 288
Db 241 LACKTAETNYCLYTVQVGLNQIKQGTGADTWSKFNKFRREMTLAVLDIIAIFPTVDPE 300

QY 289 KYPLATSVELTREIYTPDVGYSNGYWERFF--SFNSVEANGTRGPGVLVTLQAIIDYS 346
Db 301 KYPLPHVLTREIYTDVAGYSSGYSLWRNPNTENGLEANGTRGPGVLVTLWLSKIGYN 360

QY 347 HSINLQGLSWGGRHVEDFTKNGAFQRMGTSNNPRNIIFGNTDIFKIIISLARVA 406
Db 361 EYVS---RYFAGVGTGRHVEDYTKNGIFQRMGTSNNDLNIDFQNAVYKITSL---A 414

QY 407 MQPFVGYSI--PRHLVSRAEFPPTTLTFLYEVNSSGYSQ-TIESVLP-----GINKOL 457
Db 415 INVLVGETTARPEYRVSKADFRVGGPDNLNADGNNGLSRMTIESTFPLVLSHNGVR--- 471

QY 458 PPSRTNYSHRLSNAACVQNETSRVNVFGWTHTSMKKDNRIYPDKITQIPAVKAFALPACT 517
Db 472 -----GPHRLSNAACVVGNSRVNVYGTHTSLKRENIIEANQITQIPAVKSYLQNYL 526

QY 518 GVAGGYVTAGPYGTGDVVTL-----PYQA-----SLKIRLTSAPTNNKRYRLVYASGG 567
Db 527 ANAYTVVIKGT-HTGGDLIRFLTRKSEYNAVYAGGIGIRLIINNKTAGQSYRIRFRYAADK 585

QY 568 PGPFVRVSPSSVSN--ANFSRPATGG-----YSSFDYVDTLVTFNOSGVEIIION-- 618
Db 586 AAFPSVLYPGWGNRFRVLSKSYSGNYDLYKSDFKFAEITTPPLPSNSIQMDVEMQA 645

QY 619 ---LSGYHLIVDKVEFIPIDIQIEKCTKCFEGDICRCGVSQLETKEIVNSLFIN 672
Db 646 NSFQDVNVVLDKIEFLP-----SNITLLEYEGE-----RDLEKTNVANDLFTN 690

RESULT 8
US-10-782-141-20
; Sequence 20, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20

; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-20

Query Match      25.8%; Score 918.5; DB 4; Length 674;
Best Local Similarity 33.2%; Pred. No. 1.8e-71;
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY 4 MNSYQNTNEVEILLDGSNNNTMSNRYPPFAKDPNIPIN-----LDACQGRPWQDTWESV 57
Db 1 MNQYQNKNEVEILLSSQNNMNPYFPADDPNNAVMKNGNYKDWVNECEG-----SNISP 55

QY 58 SDIVTIGTYLIQFLLEPGIGGIPVFSIINKLIPSSG-----QSVAAALSICDLVSIIR 110
Db 56 SPAAATSKIVSIVLTKLAKA--VASSLADSIKSSLSIGISKITITENNVSQVSMVQVHIIIN 113

QY 111 KEYDESVLSDGVADFEGETAYQDYLYLHLEWLTDKSNPKKLADVVKQFQARBEDFTKL 170
Db 114 RRIQETILDLGESSLGLVAIYNRDYLGALAEAMNNKSNINYQNTVAEAFKTVREFFTK 173

QY 171 LAGSLRQKAEILLPTVQAAVHLLLRDAVKKYKKEWGLVCPPLYPGSGRTDCNERLK 230
Db 174 LKGIYRTSSQITLLPTTQAAVHLLSMLRDAVMYQEGWNL-----QSHINYSKELD 225

QY 231 AKIKEYTNYCVGWYKGLDQIROAGTSAEVMKSKENKFRREMTLAVLDIIAIFPTVDPEKY 290
Db 226 DALEDVTNYCEVYTTKGLNALR--GSTAIDWLEFNSPRDMLVLDLVAIFPNYPVRY 283

QY 291 PLATSVELTREIYTPDVGYSNG--NYG-W-----ERFFSFNSVEANGTRGPGVLVTLQAIID 344
Db 284 PLSTKISLSRKIYTPVGRDTSFGDWTNTGRTLANFNDLEREVTDSPSLVKWLGDMTI 343

QY 345 YHSINLQGLYSG-----WGTRHYVEDFTKNGAFQRMGTSNNPRNIIFGN---TD 395
Db 344 YTGAIIDSVRPTSPGRIGVWYGNINAFYHGTGRDVMFRQGTGDYEDPSTFISNIIYDD 403

QY 396 IFKI-----ISLARVAMQPFVGYSIIPRHLVSRAEFPPTTLTFLYEVNSSGYSQTTESV 449
Db 404 IYKLDLRAAAVSTIQAMDITFG-----VSSSRFPDIRGNQLYQSNKPYPSLPTIT 456

QY 450 LPIKNDLPPSRNTNYSHRLSNAACVQNETSRV-----NVFGWTHTSMKKDNRIYPDKI 502
Db 457 FFG-BESSSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNTILPDEI 515

QY 503 TQIPAVKAFALPACTGYAGGYVTAGPYGTGDVVTLPYQA--SLKIRLTSAPTNNKRYRVR 560
Db 516 TQIPAVTAYELRGNSS-----VVAGPGSTGGLVKMSYHVSFWSPKVCSEL---KNYRVR 567

QY 561 LRYASGCGPFRVERHSPSSVSNANFSRPATGG-----YSSFDYVDTLVTFNOSGVE 613
Db 568 IRYASHGNCQFLMKRWPSTGVAPROWARHNVQGTFSNSMEYAEAFKYLDITFITPEENFA 627

QY 614 IIIQNLSGYHLIVDKVEFIPIDIQIEKCTKCFEGDICRCGVSQLETKEIVNSLFIN 672
Db 628 FTIDLESQGLDFIDKIEFIPV-----SGSAFEGYEGKQNIKTKQAVNDLFIN 674

RESULT 9
US-10-782-096-21
; Sequence 21, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
```

; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
; FILE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274148  
; CURRENT APPLICATION NUMBER: US/10/782,096  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,633  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-096-21

Query Match 25.8%; Score 918.5; DB 4; Length 674;  
Best Local Similarity 33.2%; Pred. No. 1.8e-71;  
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;  
  
QY 4 MNSYQNTWEYELDGSNNNNMNPYPFADDPNVMKNGYKDWNECEG-----LDACQGRPWQDTWESV 57  
DB 1 MNQYQNKWEYELSSQNNNNMNPYPFADDPNVMKNGYKDWNECEG-----SNISP 55  
  
QY 58 SDIVTIGTVLIQFLPEGIGGIPVIFSIINKLIPSSG-----QSVAAISICDLVSIIR 110  
DB 56 SPAAAITSKIIVSIVLTKLAKA--VASSLADSISKSLGISTITENNVSQVSMVQVHQIIN 113  
  
QY 111 KEVDESIVLSDGVADFEGETAYQDYLYHYLEDWLTDKSNPKKLADVVKQFQAREEDFTKL 170  
DB 114 RRIQETILDGESSLGLVAIYNRDYLGALAEANNKSNINQTNVAEAFKTVREFFFTK 173  
  
QY 171 LAGSLSRQKAEILLPTVYQAAHVLLLRDVAVKYKKEWGLVCPPLYPGSGRTDCNERLK 230  
DB 174 LKGIYRTSSQITLLPTFTQAAHLHLSMLRDVAMYQEGWNL-----QSHINYSKELD 225  
  
QY 231 AKIKEYTNCVGVWYKGLDQIROAGTSABVWKNKFRREMTLAVLDIIAIPPTDYFEKY 290  
DB 236 DALEDYTNVCVETTKGLNALR--GSTAIDWLEFNSFRDMTLMVLDLVAIFPNVPVRY 283  
  
QY 291 PLATSVELTREIYDTPVGYSGG--NYG-W----ERFFSFNSVEANGTRGPGVLTWLOAIDI 344  
DB 284 PLSTKISLSRKIYDTPVGRDTPSGFDWNTGRTLANFNDLREVTDSPLVKWLGDMTI 343  
  
QY 345 YSHSINLQGLYLSG-----WGTTHYEDFTKNGAFQMSGTTNNPRNIIFGN---TD 395  
DB 344 YTGAIYSRPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTAYEDPSTFISNILDYD 403  
  
QY 396 IFKI-----ISLARYAMQPFVGYSPHILVSRAEFFPTLNTFLYEVNSSGYQSOTIESV 449  
DB 404 IYKDLRAAAVSTIQAMDITTFG-----VSSSRFFDIRGNQLQSNKPYPSLPITIT 456  
  
QY 450 LFGINKDLPPSRNTYSHRLSNAACVQNETSRV-----NVFGWTHSMKKDNRIYDPDKI 502  
DB 457 FFG-BESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNTILPDEI 515  
  
QY 503 TOIPAVKAPALPAGTYAGGYTAGPYTGDDVTLPYQA--SLKIRLSAPTNNKYRVR 560  
DB 516 TOIPAVTAYELRGNSS-----VVAGPGSTGGDLVKMSYHSVNSFKVYCSL---KNYRVR 567  
  
QY 561 LRYASGCGPFRVERWSPSSVSNANFSRPAATG-----YSSFDVYDVLVTFNQSGVE 613  
DB 568 IRYASHGNCQFLMKRWPSGVAPQWARHNVQGTFSNMRVYFAFKYLDITFTPEENFPA 627  
  
QY 614 IIIQNLSGYHLIADVKEFIPIDIQIEKCTKQCEGDCRCCEGVQSLETKKEIVNSLFIN 672  
DB 628 FTIDLESQGLFIDKIEFIPV-----SGSAFEYEGKQNIETKQKAVNDLFIN 674

RESULT 10  
US-10-782-570-17  
; Sequence 17, Application US/10782570  
; Publication No. US20040210965A1  
; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargise, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and  
; FILE REFERENCE: 045600/274144  
; CURRENT APPLICATION NUMBER: US/10/782,570  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,812  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-570-17

Query Match 25.8%; Score 918.5; DB 4; Length 674;  
Best Local Similarity 33.2%; Pred. No. 1.8e-71;  
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;  
  
QY 4 MNSYQNTWEYELDGSNNNNMNPYPFADDPNVMKNGYKDWNECEG-----LDACQGRPWQDTWESV 57  
DB 1 MNQYQNKWEYELSSQNNNNMNPYPFADDPNVMKNGYKDWNECEG-----SNISP 55  
  
QY 58 SDIVTIGTVLIQFLPEGIGGIPVIFSIINKLIPSSG-----QSVAAISICDLVSIIR 110  
DB 56 SPAAAITSKIIVSIVLTKLAKA--VASSLADSISKSLGISTITENNVSQVSMVQVHQIIN 113  
  
QY 111 KEVDESIVLSDGVADFEGETAYQDYLYHYLEDWLTDKSNPKKLADVVKQFQAREEDFTKL 170  
DB 114 RRIQETILDGESSLGLVAIYNRDYLGALAEANNKSNINQTNVAEAFKTVREFFFTK 173  
  
QY 171 LAGSLSRQKAEILLPTVYQAAHVLLLRDVAVKYKKEWGLVCPPLYPGSGRTDCNERLK 230  
DB 174 LKGIYRTSSQITLLPTFTQAAHLHLSMLRDVAMYQEGWNL-----QSHINYSKELD 225  
  
QY 231 AKIKEYTNCVGVWYKGLDQIROAGTSABVWKNKFRREMTLAVLDIIAIPPTDYFEKY 290  
DB 226 DALEDYTNVCVETTKGLNALR--GSTAIDWLEFNSFRDMTLMVLDLVAIFPNVPVRY 283  
  
QY 291 PLATSVELTREIYDTPVGYSGG--NYG-W----ERFFSFNSVEANGTRGPGVLTWLOAIDI 344  
DB 284 PLSTKISLSRKIYDTPVGRDTPSGFDWNTGRTLANFNDLREVTDSPLVKWLGDMTI 343  
  
QY 345 YSHSINLQGLYLSG-----WGTTHYEDFTKNGAFQMSGTTNNPRNIIFGN---TD 395  
DB 344 YTGAIYSRPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTAYEDPSTFISNILDYD 403  
  
QY 396 IFKI-----ISLARYAMQPFVGYSPHILVSRAEFFPTLNTFLYEVNSSGYQSOTIESV 449  
DB 404 IYKDLRAAAVSTIQAMDITTFG-----VSSSRFFDIRGNQLQSNKPYPSLPITIT 456  
  
QY 450 LFGINKDLPPSRNTYSHRLSNAACVQNETSRV-----NVFGWTHSMKKDNRIYDPDKI 502  
DB 457 FFG-BESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNTILPDEI 515  
  
QY 503 TOIPAVKAPALPAGTYAGGYTAGPYTGDDVTLPYQA--SLKIRLSAPTNNKYRVR 560  
DB 516 TOIPAVTAYELRGNSS-----VVAGPGSTGGDLVKMSYHSVNSFKVYCSL---KNYRVR 567  
  
QY 561 LRYASGCGPFRVERWSPSSVSNANFSRPAATG-----YSSFDVYDVLVTFNQSGVE 613  
DB 568 IRYASHGNCQFLMKRWPSGVAPQWARHNVQGTFSNMRVYFAFKYLDITFTPEENFPA 627  
  
QY 614 IIIQNLSGYHLIADVKEFIPIDIQIEKCTKQCEGDCRCCEGVQSLETKKEIVNSLFIN 672  
DB 628 FTIDLESQGLFIDKIEFIPV-----SGSAFEYEGKQNIETKQKAVNDLFIN 674

```
RESULT 11
US-10-783-417-15
; Sequence 15, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274146
; CURRENT APPLICATION NUMBER: US/10/783,417
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,806
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-783-417-15

Query Match      25.8%; Score 918.5; DB 5; Length 674;
Best Local Similarity 33.2%; Pred. No. 1.8e-71;
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY      4 MNSYQNTNEYEILDGSPNNMNSNRYPPFAKDPNIPFIN-----LDACQGRPMQDTWESV 57
Db      1 MNQYQNKNEYEILESSQNNMNNPNRYPPADDPNAVKNMGNYKDWNECEG-----SNISP 55

QY      58 SDIVITGYLQIFLEPGIGGIPVIFSINKLIPSSG-----QSVAAALSICDLVSIIR 110
Db      56 SPAAAITSKIVSIVLTKLAKA--VASSLADSIKSSLSGISKITITENNVSQVSMVQVHQIIN 113

QY      111 KEVDESVLSDGVADFEGETAYQDYLYHLVLEDMWLTOKSNPKKLADVVKQFQAREDEFTKL 170
Db      114 RRIQETIIDLGBESSLNGLVAIYNRDYLGALEANNKNSNINQTNVAEAFKTVREFFTK 173

QY      171 LAGSLRQKAEITLLPTVYQAAVHLLLRDVKYKKEWGLVCPPLYPGSGRTDCNERLK 230
Db      174 LKGIYRTSSQITLPTTQAAVHLLSMLRDVAVYQEGWNL-----QSHINYSKELD 225

QY      231 AKIKEYTNYCVGWYKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIFPTDYDEKY 290
Db      226 DALEDYTNVCVEVYTKGLNALR--GSTAIDWLEFNSFRDMLVLDLVAIFPNYNPVRY 283

QY      291 PLATSVELTREIYTDVPVYSGG-NYG-W-----ERPFNSVEANGTRGPGLTWLAIDI 344
Db      284 PLSTKISLSRKIYTDVPVGRDTSFGDWTNTGRTLANFNDLREVDTSPLVKWLGDMTI 343

QY      345 YSHSINLQGLVLSG-----WGTGRHYEDFTKNGAFQMSGTTSNNPNIIFGN---TD 395
Db      344 YTGALDSYRPTSPGDRIGVWYGNINAFYHTGRTDVMFQGTGDTAYEDPSTFISNILYDD 403

QY      396 IPKI-----ISLARYAMQPFVGYGIPRHLVSRABEFPPTTLNTFLYEVNSSGYSQTIESV 449
Db      404 IYKLDLRAAAVSTIQAMDITTF-----VSSSRFFDIRGNQLYQSNKPYPSLPITIT 456

QY      450 LPGAINKLPPSTNTYSHRLSNACVQNETSRV-----NVFGWTHTSKKDNRIYPDKI 502
Db      457 PFG-EESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNTILPDEI 515

QY      503 TOIPAVKAFALPAGTYAGGYVYTAGPGYTGDDVVTLPYQA--SLKIRLTSAPTNNKYRVR 560
Db      516 TOIPAVTAYELRGNS-----VVAGPGSTGGDLVVKMSHVSFWFKYVCSL---KNYRVR 567

QY      561 LRYASGPGPFPRVERWSPSSVSNANFSRPATGG-----YSSFDYVDTLVTTFNQSGVE 613
Db      568 IRYASHGNCQFLMKWEPSTGVAPROWARHNQGTFSNSNRVEAFKYLIDIFTITPENNPA 627
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QY      614 IITQNLSGYHLIVDKVEFIPIDIQIBKCTKQCEGQVQSLQETKKEIVNSLFIN 672
Db      628 FTIDLESGGDLFDKIEFIPV-----SGSAFEYEGKQNIETQKAVNDLFIN 674

RESULT 12
US-10-781-979-22
; Sequence 22, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-22

Query Match      25.8%; Score 918.5; DB 5; Length 674;
Best Local Similarity 33.2%; Pred. No. 1.8e-71;
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY      4 MNSYQNTNEYEILDGSPNNMNSNRYPPFAKDPNIPFIN-----LDACQGRPMQDTWESV 57
Db      1 MNQYQNKNEYEILESSQNNMNNPNRYPPADDPNAVKNMGNYKDWNECEG-----SNISP 55

QY      58 SDIVITGYLQIFLEPGIGGIPVIFSINKLIPSSG-----QSVAAALSICDLVSIIR 110
Db      56 SPAAAITSKIVSIVLTKLAKA--VASSLADSIKSSLSGISKITITENNVSQVSMVQVHQIIN 113

QY      111 KEVDESVLSDGVADFEGETAYQDYLYHLVLEDMWLTOKSNPKKLADVVKQFQAREDEFTKL 170
Db      114 RRIQETIIDLGBESSLNGLVAIYNRDYLGALEANNKNSNINQTNVAEAFKTVREFFTK 173

QY      171 LAGSLRQKAEITLLPTVYQAAVHLLLRDVKYKKEWGLVCPPLYPGSGRTDCNERLK 230
Db      174 LKGIYRTSSQITLPTTQAAVHLLSMLRDVAVYQEGWNL-----QSHINYSKELD 225

QY      231 AKIKEYTNYCVGWYKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIFPTDYDEKY 290
Db      226 DALEDYTNVCVEVYTKGLNALR--GSTAIDWLEFNSFRDMLVLDLVAIFPNYNPVRY 283

QY      291 PLATSVELTREIYTDVPVYSGG-NYG-W-----ERPFNSVEANGTRGPGLTWLAIDI 344
Db      284 PLSTKISLSRKIYTDVPVGRDTSFGDWTNTGRTLANFNDLREVDTSPLVKWLGDMTI 343

QY      345 YSHSINLQGLVLSG-----WGTGRHYEDFTKNGAFQMSGTTSNNPNIIFGN---TD 395
Db      344 YTGALDSYRPTSPGDRIGVWYGNINAFYHTGRTDVMFQGTGDTAYEDPSTFISNILYDD 403

QY      396 IPKI-----ISLARYAMQPFVGYGIPRHLVSRABEFPPTTLNTFLYEVNSSGYSQTIESV 449
Db      404 IYKLDLRAAAVSTIQAMDITTF-----VSSSRFFDIRGNQLYQSNKPYPSLPITIT 456

QY      450 LPGAINKLPPSTNTYSHRLSNACVQNETSRV-----NVFGWTHTSKKDNRIYPDKI 502
Db      457 PFG-EESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNTILPDEI 515

QY      503 TOIPAVKAFALPAGTYAGGYVYTAGPGYTGDDVVTLPYQA--SLKIRLTSAPTNNKYRVR 560
Db      516 TOIPAVTAYELRGNS-----VVAGPGSTGGDLVVKMSHVSFWFKYVCSL---KNYRVR 567
```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 09:48:35 ; Search time 197 Seconds  
(without alignments)  
1498.795 Million cell updates/sec

Title: US-10-782-141-3  
Perfect score: 3556  
Sequence: 1 MKNMNSYQNTNEYILDGSP.....CEGVQSLTKKKEIVNSLFIN 672

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*  
9: geneseqp2005s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3556	100.0	672	ADR89415	Adr89415 AXMI-008.
2	3540	99.6	669	ADR89417	Adr89417 AXMI-008
3	1872	52.6	666	ADR89439	Adr89439 cry40Aa1.
4	1571.5	44.2	693	ADR89402	Adr89402 AXMI-008.
5	1561.5	43.9	690	ADR89404	Adr89404 AXMI-008
6	918.5	25.8	674	ADR89435	Adr89435 cry24Aa.
7	833.5	23.4	682	ADR89408	Adr89408 AXMI-009.
8	801.5	22.5	1151	9 ABA81457	Aea81457 Bacillus
9	801.5	22.5	1156	2 AA46856	AA46856 Bacillus
10	801.5	22.5	1156	2 AA24959	AA24959 Bacillus
11	801.5	22.5	1156	3 AEA81456	Aea81456 Bacillus
12	801.5	22.5	1279	3 AAY82988	Aay82988 Native Cr
13	789.5	22.2	652	3 AAY83039	Aay83039 Cry9Aa to
14	787	22.1	656	3 AAY83040	Aay83040 Synthesis
15	782.5	22.0	671	8 ADR89410	Adr89410 AXMI-009
16	776.5	21.8	1210	5 AAU99256	AAU99256 Bacillus
17	776.5	21.8	1210	8 ADL15307	Adl15307 B thuring
18	776.5	21.8	1210	9 AEB45609	Aeb45609 B. thurin
19	776	21.8	1157	2 AAR27343	Aar27343 B.thuring
20	776	21.8	1157	2 AAR44208	Aar44208 Bacillus
21	773.5	21.8	1230	8 ADK98484	Adk98484 B thuring
22	773.5	21.8	1230	8 ADK98489	Adk98489 B thuring
23	773.5	21.8	1230	8 ADK98481	Adk98481 B thuring
24	773.5	21.8	1230	8 ADK98491	Adk98491 B thuring

25	773.5	21.8	1230	8	ADK98487	Adk98487 B thuring
26	773	21.7	1157	2	AAR28900	Aar28900 Toxin 50C
27	773	21.7	1157	2	AAR25997	Aar25997 Delta-end
28	773	21.7	1157	2	AAR33768	Aar33768 Bt isolat
29	773	21.7	1157	2	AAW06418	Aaw06418 Antiscara
30	773	21.7	1157	8	ADR89430	Adr89430 cry8Aa. 1
31	773	21.7	1157	9	ADY59865	Ady59865 Bacillus
32	772.5	21.7	1229	2	AAR54074	Aar54074 CryET5. 2
33	772.5	21.7	1229	2	AAW35259	Aaw35259 Bacillus
34	772.5	21.7	1229	2	AAW17699	Aaw17699 CryET5. 3
35	772.5	21.7	1229	2	AAW87633	Aaw87633 CryET5 pr
36	772.5	21.7	1229	2	AAW30923	Aaw30923 B. thurin
37	772.5	21.7	1229	8	ADK98479	Adk98479 B thuring
38	770.5	21.7	802	4	AAU02035	Aau02035 B. thurin
39	765.5	21.5	661	8	ADR89412	Adr89412 AXMI-009
40	765	21.5	1167	5	AAU80281	Aau80281 Bacillus
41	756.5	21.3	719	3	ABB07073	Abb07073 Bacillus
42	756.5	21.3	719	9	ADY59880	Ady59880 Bacillus
43	756.5	21.3	719	9	ADY59881	Ady59881 Bacillus
44	756	21.3	1209	4	AAU02094	Aau02094 Bacillus
45	756	21.3	1228	9	ADY59858	Ady59858 Bacillus

ALIGNMENTS

RESULT 1  
ADR89415  
ID ADR89415 standard; protein; 672 AA.  
XX AC ADR89415;  
XX DT 18-NOV-2004 (first entry)  
XX DE AXMI-008.  
XX KW delta-endotoxin; delta-endotoxin associate polypeptide;  
XX KW expression cassette; transformation; transgenic; plant; bacteria;  
XX KW lepidoptera; coleoptera; pest; pesticide; resistance;  
XX KW pesticidal activity.  
XX OS Bacillus thuringiensis.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 1 /note= "Encoded by GTG"  
XX PN WO2004074462-A2.  
XX PD 02-SEP-2004.  
XX PF 20-FEB-2004; 2004WO-US005829.  
XX PR 20-FEB-2003; 2003US-0448632P.  
XX PR 20-FEB-2003; 2003US-0448633P.  
XX PR 20-FEB-2003; 2003US-0448797P.  
XX PR 20-FEB-2003; 2003US-0448806P.  
XX PR 20-FEB-2003; 2003US-0448810P.  
XX PR 20-FEB-2003; 2003US-0448812P.  
XX PR 19-FEB-2004; 2004US-00781979.  
XX PR 19-FEB-2004; 2004US-00782020.  
XX PR 19-FEB-2004; 2004US-00782096.  
XX PR 19-FEB-2004; 2004US-00782141.  
XX PR 19-FEB-2004; 2004US-00782570.  
XX PR 19-FEB-2004; 2004US-00783417.  
XX (ATHE-) ATHENIX CORP.  
XX PA Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;  
XX PI WPI; 2004-635574/61.  
XX DR N-PSDB; ADR89413, ADR89414.



PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
XX for producing organisms with pesticide resistance.

XX Claim 12; SEQ ID NO 27; 178pp; English.

PS This sequence represents an isolated delta-endotoxin. Some of the delta-  
CC endotoxin coding sequences of the invention have alternative start  
CC codons, producing more than one protein from a single open reading frame.  
CC The nucleic acid sequences of the invention are useful in DNA constructs  
CC or expression cassettes for transformation and expression in plants and  
CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
CC killing lepidopteran or coleopteran pests. Compositions containing the  
CC delta-endotoxins of the invention, and methods for their production, are  
CC useful for the production of organisms with pesticide resistance,  
CC specifically bacteria and plants. These organisms are useful for  
CC generating altered or improved delta-endotoxin or delta-endotoxin-  
CC associated proteins that have pesticidal activity, or for detecting the  
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
CC nucleic acids in products or organisms.

XX Sequence 672 AA;

Query Match 100.0%; Score 3556; DB 8; Length 672;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKNMNSYQNTNEYEILDGSPNNTMSNRYPAKDPNIPINLDACQGRPWQWTSVSDI 60  
Db 1 MKNMNSYQNTNEYEILDGSPNNTMSNRYPAKDPNIPINLDACQGRPWQWTSVSDI 60  
Qy 61 VTIGTYLQFLLEPGIGGIPVFSIINKLIPSSGQSVAAALSCDVLVSIIRKEVDSEVLS 120  
Db 61 VTIGTYLQFLLEPGIGGIPVFSIINKLIPSSGQSVAAALSCDVLVSIIRKEVDSEVLS 120  
Qy 121 GVADPEGEMTAYQDYLYLHLEWLTDKSNPKKLADVVKQFQAREDEFTKLKAGSLSRKA 180  
Db 121 GVADPEGEMTAYQDYLYLHLEWLTDKSNPKKLADVVKQFQAREDEFTKLKAGSLSRKA 180  
Qy 181 EILLPTVYQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKIKETNYC 240  
Db 181 EILLPTVYQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKIKETNYC 240  
Qy 241 VGWTKGLDQIQAQTSAEVSKFNKFRREMTLAVLDIIAIPPTVDFEYPIATSVELTR 300  
Db 241 VGWTKGLDQIQAQTSAEVSKFNKFRREMTLAVLDIIAIPPTVDFEYPIATSVELTR 300  
Qy 301 EIYTDVPGYSGNGYGERFFNSVEANGTRGPGVLTWLQADIIYSHSINLQGLSGWG 360  
Db 301 EIYTDVPGYSGNGYGERFFNSVEANGTRGPGVLTWLQADIIYSHSINLQGLSGWG 360  
Qy 361 GTRHYEDFTKNGAFQRMSTGTTNNPNRIIFGNTDIFKIIISLARYAMOPFVGYSPRHV 420  
Db 361 GTRHYEDFTKNGAFQRMSTGTTNNPNRIIFGNTDIFKIIISLARYAMOPFVGYSPRHV 420  
Qy 421 SRABFFPTLNTFLYEVNSSGYSTIESVLPKINKDLPSPRTNYSHRLSNAACVQNETSR 480  
Db 421 SRABFFPTLNTFLYEVNSSGYSTIESVLPKINKDLPSPRTNYSHRLSNAACVQNETSR 480  
Qy 481 VNVGWTHTSMKKNRIYPDKITQIPAVKAFALPAGTGYAGGYVTAGGYTGGDVVTLPI 540  
Db 481 VNVGWTHTSMKKNRIYPDKITQIPAVKAFALPAGTGYAGGYVTAGGYTGGDVVTLPI 540  
Qy 541 QASLKIRLTSAPTKNYRVRLYASGGPGPFVERWSPSSVSNANFSPATGYSFDDV 600  
Db 541 QASLKIRLTSAPTKNYRVRLYASGGPGPFVERWSPSSVSNANFSPATGYSFDDV 600  
Qy 601 DTLVTFNQSVEIILQNSGVLHIVDKVEFIPIDIQIEKTKCFEGDICRCEGVQSL 660  
Db 601 DTLVTFNQSVEIILQNSGVLHIVDKVEFIPIDIQIEKTKCFEGDICRCEGVQSL 660  
Qy 661 TKKEIVNSLFIN 672  
|||||

Db 661 TKKEIVNSLFIN 672

RESULT 2

ADR89417  
ID ADR89417 standard; protein; 669 AA.

XX ADR89417;

DT 18-NOV-2004 (first entry)

DE AXMI-008 alternative protein.

KW delta-endotoxin; delta-endotoxin associate polypeptide;  
KW expression cassette; transformation; transgenic; plant; bacteria;  
KW lepidoptera; coleoptera; pest; pesticide; resistance;  
XX pesticidal activity.

OS Bacillus thuringiensis.

XX WO2004074462-A2.

XX 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.

XX 20-FEB-2003; 2003US-0448632P.

XX 20-FEB-2003; 2003US-0448633P.

XX 20-FEB-2003; 2003US-0448797P.

XX 20-FEB-2003; 2003US-0448806P.

XX 20-FEB-2003; 2003US-0448810P.

XX 20-FEB-2003; 2003US-0448812P.

XX 19-FEB-2004; 2004US-00781979.

XX 19-FEB-2004; 2004US-00782020.

XX 19-FEB-2004; 2004US-00782141.

XX 19-FEB-2004; 2004US-00782570.

XX 19-FEB-2004; 2004US-00783417.

XX (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

XX WPI; 2004-635574/61.

XX N-PSDB; ADR89416.

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
PT for producing organisms with pesticide resistance.

PS Claim 12; SEQ ID NO 29; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-  
CC endotoxin coding sequences of the invention have alternative start  
CC codons, producing more than one protein from a single open reading frame.  
CC The nucleic acid sequences of the invention are useful in DNA constructs  
CC or expression cassettes for transformation and expression in plants and  
CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
CC killing lepidopteran or coleopteran pests. Compositions containing the  
CC delta-endotoxins of the invention, and methods for their production, are  
CC useful for the production of organisms with pesticide resistance,  
CC specifically bacteria and plants. These organisms are useful for  
CC generating altered or improved delta-endotoxin or delta-endotoxin-  
CC associated proteins that have pesticidal activity, or for detecting the  
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
CC nucleic acids in products or organisms.

XX Sequence 669 AA;

Query Match 99.6%; Score 3540; DB 8; Length 669;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 4 MNSYQNTNEYEILDGSPNNTNMSNRYPPAKDPNIPINLDACQGRPWQDTWESVSDIVTI 63
Db 1 MNSYQNTNEYEILDGSPNNTNMSNRYPPAKDPNIPINLDACQGRPWQDTWESVSDIVTI 60
QY 64 GTYLQFLLEPGIGGIPVIFSIINKLI PSSGOSVAALSICDLVSIIRKEVDESLSGDVA 123
Db 61 GTYLQFLLEPGIGGIPVIFSIINKLI PSSGOSVAALSICDLVSIIRKEVDESLSGDVA 120
QY 124 DFEGMTAYQDYLLHYLEDWLTDKSNPKKLADVVQFOQAREEDFTKLAGSLSRQKAEIL 183
Db 121 DFEGMTAYQDYLLHYLEDWLTDKSNPKKLADVVQFOQAREEDFTKLAGSLSRQKAEIL 180
QY 184 LLPTVVOAANVHLLLRDAVKYKKGWGLVCPPLYPGSGRTDCNERLAKIKETNYVCVW 243
Db 181 LLPTVVOAANVHLLLRDAVKYKKGWGLVCPPLYPGSGRTDCNERLAKIKETNYVCVW 240
QY 244 YNKGDLQIRQAGTSAEVSKFNKFRREMTLAVLDIIAIPPTVDPEKYPLATSVELTREIY 303
Db 241 YNKGDLQIRQAGTSAEVSKFNKFRREMTLAVLDIIAIPPTVDPEKYPLATSVELTREIY 300
QY 304 TDPVYSGGNYGWERFFSFNSVEANGTRGPGGLVTLWLQADIIYSHSINLQGLYSGWGTR 363
Db 301 TDPVYSGGNYGWERFFSFNSVEANGTRGPGGLVTLWLQADIIYSHSINLQGLYSGWGTR 360
QY 364 HYEDFTKNGAFQRMSTGTTNNPRNIIFGNTDIFKII SLARYAMQPFVGYSI PRHLVSR 423
Db 361 HYEDFTKNGAFQRMSTGTTNNPRNIIFGNTDIFKII SLARYAMQPFVGYSI PRHLVSR 420
QY 424 EFPFTLNTFLYEVNSSGYSTIESVLPGINKDLPPSRNTYSHRLSNAACVQNETSRNV 483
Db 421 EFPFTLNTFLYEVNSSGYSTIESVLPGINKDLPPSRNTYSHRLSNAACVQNETSRNV 480
QY 484 FGWHTSMKKNRIYDPDKITQIPAVKAFALPAGTGAGGYTAGGYTGDDVVTLPIYQAS 543
Db 481 FGWHTSMKKNRIYDPDKITQIPAVKAFALPAGTGAGGYTAGGYTGDDVVTLPIYQAS 540
QY 544 LKIRLTSAPTNNKYRVLRYASGGPGPRVERWSPSSVSNANFSPATGYSYDFYVDTL 603
Db 541 LKIRLTSAPTNNKYRVLRYASGGPGPRVERWSPSSVSNANFSPATGYSYDFYVDTL 600
QY 604 VTTNQSQVEIIQNLSGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCEGVQSLETKK 663
Db 601 VTTNQSQVEIIQNLSGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCEGVQSLETKK 660
QY 664 EIVNSLFIN 672
Db 661 EIVNSLFIN 669
RESULT 3
ADR89439
ID ADR89439 standard; protein; 666 AA.
XX AC
XX ADR89439;
XX DT
XX 18-NOV-2004 (first entry)
XX DE
XX cry40aal.
XX KW
XX delta-endotoxin; delta-endotoxin associate polypeptide;
XX KW expression cassette; transformation; transgenic; plant; bacteria;
XX KW lepidoptera; coleoptera; pest; pesticide; resistance;
XX KW pesticidal activity.
XX OS
XX Bacillus thuringiensis.
XX EN
XX WO2004074462-A2.
XX PD
XX 02-SEP-2004.
XX PF
XX 20-FEB-2004; 2004WO-US005829.
XX XX
XX 20-FEB-2003; 2003US-0448632P.
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PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
```

(ATHE-) ATHENIX CORP.

Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

WPI; 2004-635574/61.

New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.

Example 6; SEQ ID NO 51; 178pp; English.

This sequence represents a delta-endotoxin crystal protein. This protein was included in the scope of the invention as a comparison to the delta-endotoxins of the invention. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

Sequence 666 AA;

Query Match 52.6%; Score 1872; DB 8; Length 666;

Best Local Similarity 57.0%; Pred. No. 1.3e-165; Mismatches 161; Indels 44; Gaps 15; Matches 392; Conservative 91;

```
QY 5 NSYQNTNEYEILDGSPNNTNMSNRYPPAKDPNIPINLDACQGRPWQDTWESVSDIVTI 64
Db 1 NSYENKNEYEILLESSNNTNMPNRYPPANDRDMSTMSFNDCCQGISWDEIWESAETISIG 60
QY 65 TYLIQFLLEPGIGGIPVIFSIINKLI PSSGOSVAALSICDLVSIIRKEVDESLSGDVAD 124
Db 61 IDLIEFLMEPSLGGINTLFSIIIGKLIPTNHQSVALSICDLVSIIRKEVADSLSDAICR 120
QY 125 F-EGEMTAYQDYLLHYLEDWLT-----KSNPKKLADVVQFOQAREEDFTKLAGSLSRQ 178
Db 121 FLDGKLNRYEYLLPYLEAWLKGKPLQKTNNSDIGNLVKYPFELSRRDFNEILGGSLARN 180
QY 179 KAEIILLPTVVOAANVHLLLRDAVKYKKEW-----GLVCPPLYPGSG---RTDCNER 228
Db 181 NQAILLLPYFCASCKQLLLLDADAVQYEQWPFPSAENVRSSELISPNSGCDFTGDYIER 240
QY 229 LKAKIKETNYVCVWYNKGLDQIRQAGTSAEVSKFNKFRREMTLAVLDIIAIPPTVDPE 288
Db 241 LKCKIAEVTDYCEYVWQAGLNQIKOAGTGADTWAKFNKFRREMTLAVLDIIAIPPTVD 300
QY 289 KYPLATSVELTREIYTDVPGYSGGNYGWERFF--SPNSVEANGTRGPGGLVTLWLQADII 346
Db 301 KYPLPTHVELTREIYTDVPGYSSGYTSMWKYTGAFNTLEANGTRGPGGLVTLWLSRGIYN 360
QY 347 HSNILQGLVSGWGCTRHVEDFTKNGAFQRMSTGTTNNPRNIIFGNTDIFKII SLARYA 406
```

Db 361 EYVS---RYFGWGVGTRHYEDYTTNGNFORMSGTTSNDLRDISPNSDIFKIES---KA 414  
 Qy 407 MQPFGV--YSIPRHLVSRABFPPTTLTFLFVNSSGY-SQTIESVLGINKDLPPSTN 463  
 Db 415 IMNLVGEINARPEYRVSRAEFSSESTAFYLYDAGNSGLSSMTITTSKLPFI-KNPEFSYRD 473  
 Qy 464 YSHRLSNAACVQNETSRVNVFGWTHSTMKDNRIYDPDKITQIPAVKAFALPAGTCVAGGY 523  
 Db 474 YSHRLSNAACVAGNSRNLVNGWTHSTMSKYNLIYDPDKITQIPAVKAFDI-SDTG--PGQ 530  
 Qy 524 VTAGPGYTGDDVTLTPYQASLKIRLTAPTNNKRVRLRYASGGPGPFRVERWSPSSVSN 583  
 Db 531 VIAGPGHTGNNVSLPYYSRLKIRLIPASTNKVILRVRYTSTNGRLLVERWSPSSIIN 590  
 Qy 584 ANFRPATGYSYSDYDVTLTFTNQSGVEIIQNLGYHILVDKVEFIPIDIQIEKCTK 643  
 Db 591 SYFELPSTGPGDSFGYVDVTLFTNQSGVEIIQNLDP-TPINVDKVEFIPVN-----STA 644  
 Qy 644 QPFGDICRCGVSQSLKTKKIVNSLPI 671  
 Db 645 LEYEGK-----OSLEKAQDVNDLFV 665

## RESULT 4

ADR89402  
 ID ADR89402 standard; protein; 693 AA.

XX AC ADR89402;

DT 18-NOV-2004 (first entry)

XX DE AXMI-008.

XX KW delta-endotoxin; delta-endotoxin associate polypeptide;  
 KW expression cassette; transformation; transgenic; plant; bacteria;  
 KW lepidoptera; coleoptera; pest; pesticide; resistance;  
 KW pesticidal activity.

XX OS Bacillus thuringiensis.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "Encoded by GTG"

XX WO2004074462-A2.

XX PD 02-SEP-2004.

XX PF 20-FEB-2004; 2004WO-US005829.

XX PR 20-FEB-2003; 2003US-0448632P.

XX PR 20-FEB-2003; 2003US-0448633P.

XX PR 20-FEB-2003; 2003US-0448797P.

XX PR 20-FEB-2003; 2003US-0448806P.

XX PR 20-FEB-2003; 2003US-0448810P.

XX PR 19-FEB-2004; 2004US-00781979.

XX PR 19-FEB-2004; 2004US-00782020.

XX PR 19-FEB-2004; 2004US-00782096.

XX PR 19-FEB-2004; 2004US-00782141.

XX PR 19-FEB-2004; 2004US-00782570.

XX PR 19-FEB-2004; 2004US-00783417.

XX PA (ATHE-) ATHENIX CORP.

XX PI Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;

XX DR WPI; 2004-635574/61.

XX DR N-PSDB; ADR89400, ADR89401.

XX PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 PT for producing organisms with pesticide resistance.

XX  
 PS

Claim 12; SEQ ID NO 14; 178pp; English.

This sequence represents an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, especially bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

XX Sequence 693 AA;

Query Match 44.2%; Score 1571.5; DB 8; Length 693;  
 Best Local Similarity 47.2%; Pred. No. 2.1e-137;  
 Matches 340; Conservative 107; Mismatches 198; Indels 75; Gaps 18;

Qy 1 MKWMSYQNTNEYEILDGSPNNTNMSNRYPPAKDNIPFINLDACGRPWQWTWESVDI 60

Db 1 MKKMSPYQNKNEYEILESSNNTNPNRYPFANRDMSTMWNCQGISWDEIWESVETI 60

Qy 61 VTIGTYLIQFLEPGIGIPVIFSIINKLIPSSGOSVAALSICDLVSIIRKEVDESVLSD 120

Db 61 TSGINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLVSIIRKEVADSVLSD 120

Qy 121 GVADFEGETAYQDYLLHYLEDWLT-----KSNPKKLADVVKVQFAREDEFTKLAGSL 175

Db 121 AIADPDGKLKNRYEYLVGLAWLADGKPLQKTNSDGLQVYVYKLSERDFNEILGSSL 180

Qy 176 SRQKAEIILLPTYQAAVHLLLRDAVKYKKEW-----GLVCPPLYPGSG---RTDC 225

Db 181 SRNNAQVLLPTFAQAAVQLLLRDAVQYKAWFPFLSAENVSELSIPNSGCDPTGDY 240

Qy 226 NERLAKIKETNYCVGWYKGLDOIQAAGTSAEYVSKENKPERREMTLAVLDIIAIFPTY 285

Db 241 YERLCKTAETNYCLYTWQVGLNQIKGGTADTWSKFNKFRREMTLAVLDIIAIFPTY 300

Qy 286 DFEKYPLATSVELTREIYTDVPVSGGNYGWERFF--SFNSVEANGTRGPGVLTWLQAI 343

Db 301 DFEKYPLPHTVELTREIYTDVAGYSSGYVSWLRNWPNTFNGLEANGTRGPGVLTWLSKIG 360

Qy 344 IYSHSINILQGLYSGGGTRHYEDFTKNGAFQRMGSGTTSNNPRNIIPGNTDIPKIIISLA 403

Db 361 IYNEYVS---RYFAGVGVGTRHYEDYTKNGIFQRMGSGTTSNLRNIDFQNAVYKITS- 416

Qy 404 RYAMQPFVGYSI--PRHLVSRAEFFPTTLNTLTYELVSNSSGYQ-TTESVLP-----GIN 454

Db 417 --AIMNLVGETTARPEYRVSKADPRVGGPDLNLDAGNGLSRMTIESTFPLVLHNGVR 474

Qy 455 KDLPSRTNYSRLSNAACVQNETSRVNVFGWTHSTMKDNRIYDPKIQIPAVKAFALP 514

Db 475 -----GPHRLSNAACVYGVNVRVYGVGTHSTLKENIEANQIQIPAVKSYLQ 526

Qy 515 AGTGYAGGYVTAAGPYTGDDVVTL-----PYQA-----SLKRLTSAPTNKNRVRLRYA 564

Db 527 NYLANAYTVIKGT-HTGGDLIRFLRTKSEYNAVAGGGIRLIINNKTAGSQSYRIFRYA 585

Qy 565 SCGPFPFRVERWSPSSVSN--ANFSRPATGG-----YSSFDYVDVTLVTFNQSGVILIQ 617

Db 586 ADKAAFFSVLYPGGWSNRFVSLKSYSGNVDLLKYSDFKFAEIIITPPLPSSNIQMDVE 645

Qy 618 N-----LSGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCEGVQSLETKKEIVNSLFIN 672

Db 646 MQANSFQSDVNVVLDKIEFLP-----SNVTILEYEGE-----RDEKTKNAVNDLFTN 693

## RESULT 5

ADR89404  
 ID ADR89404 standard; protein; 690 AA.  
 XX ADR89404;  
 AC ADR89404;  
 XX 18-NOV-2004 (first entry)  
 DT  
 DE AXMI-008 alternative protein.  
 XX delta-endotoxin; delta-endotoxin associate polypeptide;  
 KW expression cassette; transformation; transgenic; plant;  
 KW lepidoptera; coleoptera; pest; pesticide; resistance;  
 KW pesticidal activity.  
 XX Bacillus thuringiensis.  
 OS  
 XX WO2004074462-A2.  
 PN  
 XX 02-SEP-2004.  
 PD  
 XX 20-FEB-2004; 2004WO-US005829.  
 PF  
 XX 20-FEB-2003; 2003US-0448632P.  
 PR  
 XX 20-FEB-2003; 2003US-0448633P.  
 PR  
 XX 20-FEB-2003; 2003US-0448797P.  
 PR  
 XX 20-FEB-2003; 2003US-044806P.  
 PR  
 XX 20-FEB-2003; 2003US-0448810P.  
 PR  
 XX 19-FEB-2004; 2004US-007812P.  
 PR  
 XX 19-FEB-2004; 2004US-0078197P.  
 PR  
 XX 19-FEB-2004; 2004US-0078202P.  
 PR  
 XX 19-FEB-2004; 2004US-0078209P.  
 PR  
 XX 19-FEB-2004; 2004US-0078214P.  
 PR  
 XX 19-FEB-2004; 2004US-0078257P.  
 PR  
 XX 19-FEB-2004; 2004US-00783417.  
 XX  
 PA (ATHE-) ATHENIX CORP.  
 XX  
 XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
 PI N-PSDB; ADR89403.  
 DR WPI; 2004-635574/61.  
 DR N-PSDB; ADR89403.  
 XX  
 PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 PT for producing organisms with pesticide resistance.  
 XX  
 PS Claim 12; SEQ ID NO 16; 178pp; English.  
 XX  
 CC This sequence represents an isolated delta-endotoxin. Some of the delta-  
 CC endotoxin coding sequences of the invention have alternative start  
 CC codons, producing more than one protein from a single open reading frame.  
 CC The nucleic acid sequences of the invention are useful in DNA constructs  
 CC or expression cassettes for transformation and expression in plants and  
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
 CC killing lepidopteran or coleopteran pests. Compositions containing the  
 CC delta-endotoxins of the invention, and methods for their production, are  
 CC useful for the production of organisms with pesticide resistance,  
 CC specifically bacteria and plants. These organisms are useful for  
 CC generating altered or improved delta-endotoxin or delta-endotoxin-  
 CC associated proteins that have pesticidal activity, or for detecting the  
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
 CC nucleic acids in products or organisms.  
 XX  
 SQ Sequence 690 AA;

Query Match 43.9%; Score 1561.5; DB 8; Length 690;  
 Best Local Similarity 47.1%; Pred. No. 1.8e-136;  
 Matches 338; Conservative 107; Mismatches 197; Indels 75; Gaps 18;  
 Qy 4 MNSYONTNEYELDGSPPNNTNMSNRYPPAKDNPFPINLDACQGRPWQDTWESVDIVTI 63  
 Db 1 MSPYQNKNEYELLESNNNTNPNRYPPANNRDMSTMSWNCQGISWDEIWESVETITSI 60

QY 64 GTYLIOFLLEPGIGGIPVIFSIINKLIPSSQSVAAALSICDLVSIIRKEVDSEVLSDGVA 123  
 DB 61 GINLIEFVIEPSIGGINLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIA 120  
 QY 124 DFEGMTAYODYLHYLEDWLT-----KSNPKKLADVVKQFOAREEDFTKLGLSLRQ 178  
 DB 121 DFDGKLKNRYEYLYSLGAWLKDGPLOKTNNSDIGQLVYVFKLSERDFNEILGSLSRN 180  
 QY 179 KAEIILLPTVQAAVHLLLRDAVKYKKEW-----GLVCPPLYPGSG---RTDCNER 228  
 DB 181 NAQVLLLPFAQAANVQLLRDAVQYKAQWFPFLSAENVRSELISPSNGCDFTGDYDER 240  
 QY 229 LKAKIKEYTNYCVGWYNGKLDQIRQACTSAEVSKFNKFRREMTLAVLDIIAIPPTDYFE 288  
 DB 241 LKCKTAYTNYCLYQVGLNQIKGGTGADTWSKFNKFRREMTLAVLDIIAIPPTDYFE 300  
 QY 289 KYPLATSVELTREIYTDVPGYSGNYGWERFF--SFNSVEANGTRGPGLVTLQALDIYS 346  
 DB 301 KYPLPHTVELTREIYTDVAGYSSGYTSMWRNWPNTFNGLEANGTRGPGLVTLWSKIGYN 360  
 QY 347 HSINLOGLYLSGCGTRHYEDFTKNGA FORMSGTTNNPNRIIFGNTDIFKILSLARYA 406  
 DB 361 EYVS---RYFAGWVGTRHYEDYTKNGIFORMSGTTNDLRNIDFNADVYKITSLS---A 414  
 QY 407 MQPFFVGYSI--PRHLVSRAEFFFTLTNTFLYEVNSSGYSQ-TIESVLP-----GINKDL 457  
 DB 415 IMNLVGETTARPEYRVSKADFRVGGPDLDYDAGNGLSRMTIESTPPLVLHSGNVR--- 471  
 QY 458 PPSRTNYSRLSNAACVQNETSRVNVFGWTHSMKKDNRIYDPDKITQIPAVKAFALPAGT 517  
 DB 472 ----GPHRLSNAACVYGVNSRVNVGWTHSLKRENIIEANGITQIPAVKSYLYQNL 526  
 QY 518 GYAGGYVTAGPGYTGDDVVTL-----PYQA-----SLKIRLTSAPTKNYRVRURYASGG 567  
 DB 527 ANAYTVIKGT-HTGGDLIRFLRTKSEYNAVAGGGIRLIINNKTAGQSYRIRFRYAADK 585  
 QY 568 PGFPRVERMSPSVSN--ANFSRPATGG-----YSPFDYVDVTLVTTNQSQVEIILQN-- 618  
 DB 586 AAFPSVLYPGGWSNRFSLEKSYSGNYDLDKYSDFKFAEIIITPPLPSSNIQMDVENQA 645  
 QY 619 ---LSGYHLIVDKVEPIPIQIEKTKQCFDRCGVSQSLTKKEIVNSLFIN 672  
 DB 646 NSFQSDVNVLDKIEFLP-----SNTTLEYEGE-----RDLEKTKNAVNDLFTN 690

## RESULT 6

ADR89435  
 ID ADR89435 standard; protein; 674 AA.  
 XX ADR89435;  
 AC ADR89435;  
 XX 18-NOV-2004 (first entry)  
 DT  
 DE cry24Aa.

XX delta-endotoxin; delta-endotoxin associate polypeptide;  
 KW expression cassette; transformation; transgenic; plant; bacteria;  
 KW lepidoptera; coleoptera; pest; pesticide; resistance;  
 KW pesticidal activity.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO2004074462-A2.  
 PD  
 XX 02-SEP-2004.  
 XX  
 XX 20-FEB-2004; 2004WO-US005829.  
 PF  
 XX 20-FEB-2003; 2003US-0448632P.  
 PR  
 XX 20-FEB-2003; 2003US-0448633P.  
 PR  
 XX 20-FEB-2003; 2003US-0448797P.  
 PR  
 XX 20-FEB-2003; 2003US-0448806P.

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PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX (ATHE-) ATHENIX CORP.
XX
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.
XX
XX Example 6; SEQ ID NO 47; 178pp; English.
XX
XX This sequence represents a delta-endotoxin crystal protein. This protein
XX was included in the scope of the invention as a comparison to the delta-
XX endotoxins of the invention. Some of the delta-endotoxin coding sequences
XX of the invention have alternative start codons, producing more than one
XX protein from a single open reading frame. The nucleic acid sequences of
XX the invention are useful in DNA constructs or expression cassettes for
XX transformation and expression in plants and bacteria. The nucleic acids
XX and corresponding polypeptides are useful for killing lepidopteran or
XX coleopteran pests. Compositions containing the delta-endotoxins of the
XX invention, and methods for their production, are useful for the
XX production of organisms with pesticide resistance, specifically bacteria
XX and plants. These organisms are useful for generating altered or improved
XX delta-endotoxin or delta-endotoxin-associated proteins that have
XX pesticidal activity, or for detecting the presence of delta-endotoxin or
XX delta-endotoxin-associated proteins or nucleic acids in products or
XX organisms.
XX
XX Sequence 674 AA;
XX
XX Query Match 25.8%; Score 918.5; DB 8; Length 674;
XX Best Local Similarity 33.2%; Pred. No. 3.5e-76;
XX Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;
XX
XX 4 MNSYQNTNEYILDGSPNNTNMSNRYPAKDPNIPIN-----LDACQRPQDWTSV 57
XX 1 MNQYQNKNEYILESSQNNMNPYPFADDPNAVKNMGNYKDWNECEG-----SNISP 55
XX
XX 58 SDIVTIGYILQFLPGLGIGGIPVIFSIINKLIPSG-----QSVAAISICDLVSIIR 110
XX 56 SPAAAITSKIIVSIVLKTAKA--VASSLADSIKSLIGISKITITENNVSQVSVQVHQIIN 113
XX
XX 111 KEVDSVLSGDVADPEGETAYQDYVLYHLEDLTKGNPKKLADVVKQFOAREEDFTKL 170
XX 114 RRIQETILDGSSINGLVAIYNRDYLGALEANNKNSINQTNVAEAFKIVREFFTK 173
XX
XX 171 LAGLSRQKAEILLPTTYVQAAVNHLLLRDRAVYKKKEMGLVCPPLPGSGRTDCNERLK 230
XX 174 LKGIYRTSSSQITLPTTQAAANLHLSMLRDVAVMYQEGWNL-----QSHINYSKELD 225
XX
XX 231 AKIKEYTYCVGWYKGLDQIRQAGTSABVWSKFNKPREMTLAVLDIIAIFPTDYFKY 290
XX 226 DALEDYTYNCEVYTKGLNALR--GSTAIDWLEFNSFRDMLTLMVLDLVAIFPNVPVRY 283
XX
XX 291 PLATSVELTREIYTPVGVSGG--NYG-W-----ERFESFNSVEANGTRGGLVTLWQAIDI 344
XX 284 PLSTKISLSRKIYTPDVGKTDSPFGDWTNTGRTLANFNDLEREVDTSFLVNLGDMTI 343
XX
XX 345 YSHSINLQGLYLSG-----WGTGRHYEDFTKNGAFAORMSGTTSNNPRNIIFGN---TD 395
XX 344 YTGADSVRPTSPGRIGVWYGNINAFYHTGRTDVVMFPQTGDTAYEDPSTFISNLYDD 403
XX 336 IFKI-----ISLARYAMQPFVGYISIPRHLVSRARFFPTTLNLTFLYEVNSSGYSQTIESV 449

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Db 404 IYKDLRAAAVSTIQGAMDTTF-----VSSRFDIRGRNQLQSNKPYPSLPTIT 456
QY 450 LPIGINKDLPSPRTNYSRLSNAAVCQNETSRV-----NVFGWTHTSMKKNRIYDPDKI 502
Db 457 FPG-BESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNTILPDEI 515
QY 503 TOIPAVKAFALPAGTGYAGGYVTAGPGYTGDDVVTLPYQA--SLKRLTSAPTNKNRYVR 560
Db 516 TOIPAVTAYELRGNSS-----VVAGPGSTGGDLVKMSYHSVMSFKVYCSL---KNRYVR 567
QY 561 LRYASGGPGPFRVERWSPSSVSNANFSRPAATG-----YSSFYVDVTLVTTFNOSGVE 613
Db 568 IRYASHGNCQFLMKRWPSGTGVAPQWRAHNVQTFSNSMRYEAFKYLIDFTITPENNFA 627
QY 614 IILQNLGSHLIVDKVEFIPIDIQIEKTKCFEGDICEGVSQSLTKKEIVNSLFIN 672
Db 628 FTIDLESGDGLFDIKIEFIPV-----SGSAFEYEGKQNIETKQKAVNDLFIN 674

```

## RESULT 7

ADR89408

ID ADR89408 standard; protein; 682 AA.

XX AC ADR89408;

XX DT 18-NOV-2004 (first entry)

XX DE AXMI-009.

XX KW delta-endotoxin; delta-endotoxin associate polypeptide;

XX KW expression cassette; transformation; transgenic; plant; bacteria;

XX KW lepidoptera; coleoptera; pest; pesticide; resistance;

XX KW pesticidal activity.

XX OS Bacillus thuringiensis.

XX PN WO200407462-A2.

XX PD 02-SEP-2004.

XX PF 20-FEB-2004; 2004WO-US005829.

XX PR 20-FEB-2003; 2003US-0448632P.

XX PR 20-FEB-2003; 2003US-0448633P.

XX PR 20-FEB-2003; 2003US-0448797P.

XX PR 20-FEB-2003; 2003US-0448806P.

XX PR 20-FEB-2003; 2003US-0448810P.

XX PR 20-FEB-2003; 2003US-0448812P.

XX PR 19-FEB-2004; 2004US-00781979.

XX PR 19-FEB-2004; 2004US-00782020.

XX PR 19-FEB-2004; 2004US-00782096.

XX PR 19-FEB-2004; 2004US-00782141.

XX PR 19-FEB-2004; 2004US-00782570.

XX PR 19-FEB-2004; 2004US-00783417.

XX (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

XX WPI; 2004-635574/61.

XX N-PSDB; ADR89407.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids

XX and polypeptides, useful for killing lepidopteran or coleopteran pests or

XX for producing organisms with pesticide resistance.

XX PS Claim 12; SEQ ID NO 20; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-

XX endotoxin coding sequences of the invention have alternative start

XX codons, producing more than one protein from a single open reading frame.

XX The nucleic acid sequences of the invention are useful in DNA constructs

or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

XX Sequence 682 AA;

Query Match 23.4%; Score 833.5; DB 8; Length 682;  
 Best Local Similarity 33.8%; Pred. No. 3.4e-68;  
 Matches 257; Conservative 112; Mismatches 222; Indels 169; Gaps 40;

QY 4 MNSYQNTNEYEILDSPNNTMSN---RYPPAKDPNIPFINDACQGRPWQDTWES-----56  
 DB 1 MNSYKNQNEYEMLDALRINSNSNCYPRYFLAKDPQMTWRNTNY---KEWLNNCDSNTQF 57  
 QY 57 VSDIVT-----IGTYLIQFLLEPGIGPVI---FSIINKLI---90  
 DB 58 IGDISTYSPEALSVRDALFGINSVGTLSNL-----GVPLASQSGFIISRLIGIL 110  
 QY 91 ---PSSGQSVAAISICDLVSIIRKEVDSVLSDGVADPEGEMTAYDYLHYLEDWLTDK 147  
 DB 111 WAGPDPFFALMWL-----VEELIKSIDQVRNALRELEG-IQIMRLYQTRLOAWLVNK 165  
 QY 148 SNPKKLADVVKQFQAREEDFTKLAGLSRQKAEILLFTYVQAAVHLLLRDVAKYKK 207  
 DB 166 NDDNRRRA-LVTQYAVDNFFEKMP-KPKERNEIILLFPVYQAANLHILLRDADYFCA 223  
 QY 208 EWGLVCPPLYPGSGTDCNE---RLKAKIKEYNTVCVWYNGKGLDQIRQAGTSAEWSKF 264  
 DB 224 QMWL-----GDDEIRDNYIRLQGLIREYKDHCHITFYNQGLNQFNR--SNAQDWVSF 272  
 QY 265 NKFRREMTLAVLDIIAIPPTDYFEKYPLATSVELTREIYTPVGY-----SGS-NYGM-- 316  
 DB 273 NFRFTDMTLVLDLAILFPNDPRYPYLAVKTELTREYTPDVGTVLESGRGYIPWYN 332  
 QY 317 ERFFSFNSVEANGTRPGVLTVLQALDIYSHSINLQGLYLSQGGTGRHYEDFTKNGARFQ 376  
 DB 333 PNNTFTAMENNARRPSYTTWLNRI FVYTRTLGNMSDVRTNGGHTLVENGNDGSEITH 392  
 QY 377 RMSGTTSNP-RNIIFGNTDIPKISLARYAMQPFVG-----YSIPRHLVSRABFFPT 429  
 DB 393 NFGKTDSTIPQYFNANLSVESISLARI-----YLGTEANNYITSOYGVSRVIFNTSN 448  
 QY 430 LN-----TFLYEVNSSGYSTIESVLPGLNKDLP-PSRTNYSHLSNAACVQNETSR---- 480  
 DB 449 INNVPGSLRYEPALPQSOTISELPG--KKPRNAGDFSHRLS---YISNFDARRSSS 503  
 QY 481 ----VNVFGWTHSMKDNRIYDPKIQTQIPAKAFALPAGTGYAG--GYVTAGPGYTG 533  
 DB 504 GGIIVSLTFGWAHTSMRNLRLPKITQIDAVK-----GWGNGTGFVIPGP--TGG 553  
 QY 534 DVVTLPYQ-ASLKIRLTSAPTNKNYRVLRYA---SGGPGPFRVRWSPSSV-----SN 583  
 DB 554 NLVKVSDMSHSLKVQAPQRT--SYRILRYACLVTHGDAIF-VEHSGSSHIVSFPDCSN 610  
 QY 584 ANFSRPA-TGGYSFDDYDT-----LVTTFNQSGVEIILQNLGGYHLIVDKVEFI 632  
 DB 611 SS-GRPSNTLLESDDRYIDVPGIFTSPINLIYRTQS-----FGTHAI-DKFEFI 659  
 QY 633 PIDIQIEKCTKQFEGDICRCEGVOSLETKEIIVNSLFN 672  
 DB 660 PLN-----TFPN-----OSLEKREOVNDLFN 682

RESULT 8

AEA81457

ID AEA81457 standard; protein; 1151 AA.

XX AEA81457;  
 AC 25-AUG-2005 (first entry)  
 DT Bacillus thuringiensis Cry9 protein, cryaa2, SEQ ID NO: 13.  
 DE Transgenic plant; pesticide; genetically engineered microorganism; cry9;  
 KW endotoxin.  
 XX Bacillus thuringiensis.  
 OS US2005138685-A1.  
 PN 23-JUN-2005.  
 PD 21-DEC-2004; 2004US-00018615.  
 PF 22-DEC-2003; 2003US-0531807P.  
 PR (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA Flannagan RD, Abad AR;  
 PI WPI; 2005-444221/45.  
 DR New isolated nucleic acid encoding a polypeptide having pesticidal  
 PT activity, useful for controlling pests, especially plant pests such as  
 PT European corn borer, diamond-back moth or fall armyworm.  
 XX Disclosure; SEQ ID NO 13; 114pp; English.  
 PS The present invention relates to the Bacillus thuringiensis Cry9-family  
 CC genes that encode delta-endotoxins having pesticidal activity against  
 CC insect pests. The invention is useful for producing pesticidal  
 CC compositions for controlling pests in plant such as European corn borer,  
 CC diamond-back moth or fall armyworm. The invention is also useful in  
 CC production of transgenic plant. The present sequence is the Bacillus  
 CC thuringiensis Cry9 protein.  
 XX Sequence 1151 AA;

Query Match 22.5%; Score 801.5; DB 9; Length 1151;  
 Best Local Similarity 31.2%; Pred. No. 8.2e-55;  
 Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;

QY 9 NTNEYELDGPNNNTMSN---RYPPAKDPNIPFINDACQGRP---WQD-TWESVSDIV 61  
 DB 2 NQKHGII-GASCGCASDDVAKYPLANNPYSSALNLSQNSILNWINIIGDAAKEAV 60  
 QY 62 TGTGTYLIQFLLEPGIGG-IPVIFSIINKLI-PSSGQSVAAALSTCDLVIIRKEVDESVL 119  
 DB 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGGSSQSISDLSCDLLSIIDLRVSQSVLN 120  
 QY 120 DGVADPEGEMTAYDYLHYLEDWLTDKSNPKLA--DVVKQFQAREEDFTKLL----- 171  
 DB 121 DGIADFNQSVLLYRN-YLEALDSW---NKNPNSASABELRTRPRIADSEFDRILTRGSLT 176  
 QY 172 -AGLSRQKAEILLPTVYQAAVHLLLRDVAKYKKEWGLVCPPIYPGSGRDTDCNRLK 230  
 DB 177 NQGSILARQNAQIILLPSPASAAFFHLLLRDTRATRYGTNWG-----LYNATPFNYQSKLV 231  
 QY 231 AKIKYTYNVCVWYNGKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIPPTDYFEKY 290  
 DB 232 ELIELYTDYCVHWYNGRNFELRQRTSATAWLEFHYRREMTLWLDIVASFSSLDITNY 291  
 QY 291 PLATSVELTREIYTPVGY-----SGGNYQWERFF---SFSNVEANGTRGGLVTLWQALD 343  
 DB 292 PIETDFQLSRVYITDPIGFVHRSSLRGSEWFSFVRNANFSDLF-NAIPNPRPSWFLNNMI 350  
 QY 344 IYSHSINILQGLVLSG-----WGGTRHYEDFTKNGAF--QRMSCTTSNNPRNIIFGNTDIF 397  
 DB 351 ISTGSLTLPVSPSTDRARVWYGSR---DRISPAHQITELISQHTTATQITLGRN--IF 406

QY 398 KIISLARYAMQPFVCGYSIPRHLVSRAEPPTT---LNTFLYE--VNSSGYS-----QTIES 448  
 DB 407 RVDSQACMLNDTTYG-----VNRVAFYHDASEGSRQSVYEGYRTTGIDNPRVQNIPT 459  
 QY 449 VLPGLKDLPPSRNTYSHRLSNA-----ACVQNETSRVNVFGWTHTSMMKKNRIYDP 500  
 DB 460 YLPGNSDI-PPEDYTHILSTINLTGGLRQVANSRRSSLYMGWTHKSLARNNTINPD 518  
 QY 501 KITQIPAVKAFALPAGTGYAGGYTAGGYTGDDVWTLPYQASLKIRLSAPT--KNYR 558  
 DB 519 RITQIPLTKVDTRGTGVSYN-----DPGFIGGALLQRTDHGSLGVLRVQFPLHLRQQYR 573  
 QY 559 VRLRYASGGPGPFRVERWSPSSVSNANFSRPAT-----GGYSSFDYDVLVTTFNQ 609  
 DB 574 IRVRYAS-----TTNIRLSVNGSFGTISQNLPTMRLGEDLRYGSAIREFNTSIRPTASP 629  
 QY 610 SGVEIIIO-NLSGYHLIVDKVEFIPIDIQIEKCTKQPEGDICRCBGVQSLETKKEIVNS 668  
 DB 630 DQIRLTIEPSFIRQEVYDRIEFIPVN-----PTR-----EAKEDLEAAKAVAS 674  
 QY 669 LF 670  
 DB 675 LF 676

RESULT 9  
 AAW46856  
 ID AAW46856 standard; protein; 1156 AA.  
 XX  
 AC AAW46856;  
 XX  
 DT 11-JUN-1998 (first entry)  
 XX  
 DE Bacillus thuringiensis toxin designated 86BB1(a).  
 XX  
 KW Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;  
 KW Heliothis virescens; Helicoverpa zea.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO9800546-A2.  
 XX  
 PD 08-JAN-1998.  
 XX  
 PF 01-JUL-1997; 97WO-US011658.  
 XX  
 PR 01-JUL-1996; 96US-00674002.  
 XX  
 PA (MYCO ) MYCOGEN CORP.  
 XX  
 XX Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;  
 FI  
 XX WPI; 1998-086971/08.  
 DR N-PSDB; AAV16515.  
 DR  
 XX  
 PT New isolated Bacillus thuringiensis isolate(s) - used to obtain genes  
 PT encoding toxins which are active against lepidopteran pests such as the  
 PT Black cutworm.  
 XX  
 PS Claim 34; Page 82-86; 183pp; English.  
 XX  
 CC The present sequence represents a Bacillus thuringiensis toxin designated  
 CC 86BB1(a) which is active against lepidopteran pests. The toxin isolates  
 CC can be used for the control of lepidopteran pests such as Agrotis ipsilon  
 CC (black cutworm), Heliothis virescens and Helicoverpa zea. PCR primers and  
 CC probes can be derived from the polynucleotide encoding the toxin and used  
 CC for the amplification and detection of other toxin-encoding sequences  
 XX  
 SQ Sequence 1156 AA;

Query Match 22.5%; Score 801.5; DB 2; Length 1156;  
 Best Local Similarity 31.2%; Pred. No. 8.2e-65;

Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;  
 QY 9 NTNEYIILGSPNNTMSN---RYFPKDPNTPFPNLDACQGRP---WQD-TWESVSDIV 61  
 DB 2 NQMKGII-GASNCOCASDDVAKYPLANNPYPSALNLSQNSILLNWINIIGDAAKEAV 60  
 QY 62 TIGTYLIQFLLEPGIGG-IPVIFSIINKLI-PSSGQSAALSCIDLVSIIRKEVDSVLS 119  
 DB 61 SIGTTIVSLITAPSTGLISIVIDLIGKVLGSSGQISDLSICDLSIIDLRVSQVLN 120  
 QY 120 DGVADEGEEMTAYQDYIHLHLEDWLTDSNPKKLA--DVVKQFOAREEDFTKLL----- 171  
 DB 121 DGIADFNGLVLLYRN-YLEALDSW---NKNPNSASAEELRTRFIADSEFDRLITRGSLT 176  
 QY 172 -AGSLSRQKAEILLPTTVYQAAANVHLLLRDQVKKWGLVCCPPIYPSGRTDCNERLK 230  
 DB 177 NGGSLARQNAQIILLPSFASAAFFHLLLRDQVKKWGLVCCPPIYPSGRTDCNERLK 231  
 QY 231 AKIKEYTVYCVGMYNKGDLQIRQAGTSAEVSKENKFRREMTLAVLDIITAIPTTYDEKY 290  
 DB 232 ELIELYTDYCVHWYNRGFGNELQRGTSATAWLEFHRYREMTLWLDIVASFSSLDITNY 291  
 QY 291 PLATSVELTREIYTDVPGY---SGNYGWERFF---SPNSVEANGTRGFLVTLQAD 343  
 DB 292 PIETDFQLSRVYITDPIGFVHRSSLRGESWFSFVNANFSDLLE-NAIPNPSWFLNNMI 350  
 QY 344 IYSHSINLQGLYLG---WGTRHYEDFTKNGAP--QRMSTGTTNNPRNIIFGNTDIF 397  
 DB 351 ISTGSLTLVPSPTDRARVWYGSR--DRISPANSQFITEILISGQHTTATQTLGRN--IF 406  
 QY 398 KIISLARYAMQPFVCGYSIPRHLVSRAEPPTT---LNTFLYE--VNSSGYS-----QTIES 448  
 DB 407 RVDSQACMLNDTTYG-----VNRVAFYHDASEGSRQSVYEGYRTTGIDNPRVQNIPT 459  
 QY 449 VLPGLKDLPPSRNTYSHRLSNA-----ACVQNETSRVNVFGWTHTSMMKKNRIYDP 500  
 DB 460 YLPGNSDI-PPEDYTHILSTINLTGGLRQVANSRRSSLYMGWTHKSLARNNTINPD 518  
 QY 501 KITQIPAVKAFALPAGTGYAGGYTAGGYTGDDVWTLPYQASLKIRLSAPT--KNYR 558  
 DB 519 RITQIPLTKVDTRGTGVSYN-----DPGFIGGALLQRTDHGSLGVLRVQFPLHLRQQYR 573  
 QY 559 VRLRYASGGPGPFRVERWSPSSVSNANFSRPAT-----GGYSSFDYDVLVTTFNQ 609  
 DB 574 IRVRYAS-----TTNIRLSVNGSFGTISQNLPTMRLGEDLRYGSAIREFNTSIRPTASP 629  
 QY 610 SGVEIIIO-NLSGYHLIVDKVEFIPIDIQIEKCTKQPEGDICRCBGVQSLETKKEIVNS 668  
 DB 630 DQIRLTIEPSFIRQEVYDRIEFIPVN-----PTR-----EAKEDLEAAKAVAS 674  
 QY 669 LF 670  
 DB 675 LF 676

RESULT 10  
 AAY24959  
 ID AAY24959 standard; protein; 1156 AA.  
 XX  
 AC AAY24959;  
 XX  
 DT 09-SEP-1999 (first entry)  
 XX  
 DE Bacillus thuringiensis toxin 86BB1(a).  
 XX  
 KW Bacillus thuringiensis; toxin; Ostrinia nubilalis; lepidopteran;  
 KW European corn borer; black cutworm.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO9933991-A2.  
 XX  
 PD 08-JUL-1999.

XX 15-DEC-1998; 98WO-US026585.  
XX 31-DEC-1997; 97US-00002285.  
XX (MYCO) MYCOGEN CORP.  
XX  
PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;  
PI Muller-Cohn J;  
DR WPI: 1999-405513/34.  
DR N-PSDB; AX83876.  
XX  
XX Method for control of European corn borer using *Bacillus thuringiensis*  
toxins.  
XX  
XX Claim 1; Page 86-90; 174pp; English.  
XX  
CC A method has been developed for the control of European corn borer  
CC (*Ostrinia nubilalis*), comprising contacting the pest with a pesticidal  
CC amount of a *Bacillus thuringiensis* toxin. The method is used for the  
CC control of European corn borer (*Ostrinia nubilalis*). The method can also  
CC be used for the control of other non-mammalian pests, particularly black  
CC cutworm, and other lepidopteran pests. The present sequence represents a  
CC *Bacillus thuringiensis* toxin from the present invention  
XX  
SQ Sequence 1156 AA;  
  
Query Match 22.5%; Score 801.5; DB 2; Length 1156;  
Best Local Similarity 31.2%; Pred. No. 8.2e-65;  
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;  
  
QY 9 NTNEYILDGSPNNTMNSN---RYFPKDPNIPFNLDACQGRP---WQD-TWESVSDIV 61  
DB 2 NONKHGII-GASNCGCASDDVAKYPLANNPYSSALNLSQNSSLNINIIGDAAKEAV 60  
  
QY 62 TIGTVLIQFLLEPGIGG-IPVIFSIINKLI-PSSGOSVAALSICDLVSIIRKEVDESVL 119  
DB 61 SIGTTIVSLITAPSLTGLISIVDILGKVLGSSGQSISDLSICDLSSIILDRVSQSVLN 120  
  
QY 120 DGVADPEGEMTAYQDYLYLHLEDWLTDKSNPKKLA--DVVKQFOAREEDFTKLL----- 171  
DB 121 DGIADFNGLSVLLYRN-YLEALDSW---NKNPNSASAEELTRFRIADSEDFRILTRGSLT 176  
  
QY 172 -AGLSLRQKAEILLPTVQAAVHLLLRDVAKYKKGWGLVCPPLYPGSGRTDCNERLK 230  
DB 177 NGGSLARQNAQILLPSPASAFFHLLLRDTRATRYGTNWG-----LYNATPPINYSQSLV 231  
  
QY 231 AKIKETNYCVGWYNGKLDQIRQAQTSAEVMSKFNKEREMTLAVLDIIAIFPTDYFEKY 290  
DB 232 ELIELYDTCVHWYNRGNEQLRQRTSATAMLEFHYRREMTLMVLDIVASFSSJDTNY 291  
  
QY 291 PLATSVELTREIYTPDVGY---SGCNYGWERFF---SFNSVEANGTRGPGIWTWLQALD 343  
DB 292 PIETDFQLSRVITYTDPDGFVHRSSLRGESWFSFVNANFSDLN-NAIPNPSFWELNNMI 350  
  
QY 344 IYSHINILQGLVSG-----WGTRHYEDFTKNGAF--QRMSGTTSNNPRNIIFGNTDIF 397  
DB 351 ISTGSLTLVPSPSTDRARVWYGSR--DRISPANSQFITEILISQHTTATQTLILGRN--IF 406  
  
QY 398 KIISLARVAMPQFVGYSPHRLVSAEFPPTT--LNTFLYE--VNSSGYS-----OTIES 448  
DB 407 RVDQOACNLNDTTYG-----VNRAPVYHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459  
  
QY 449 VLPGLINKDLPSPRTNYSHRLSNA-----ACVQNETSRVNVFGWTHTSMMKDNRIYPD 500  
DB 460 YLPGENSDI--TPEDYTHILSTTINLTGGLQVANSRRSSLLVMYGTWTHKSLARNNTINPD 518  
  
QY 501 KITQIPAVKALPAGTYAGGYVTAGPYCTGGDVVTLFPYQASLKIRLTSAFTN--KNYR 558  
DB 519 RITQIPLTKVDRTRGTGVSVMN-----DFGFIGALLQRTDHGSLGLVLRVQFPLHLRQYR 573  
  
QY 559 VRLRYASGPGPFRVERWSPSVSNANFSRPAT-----GGYSSFDYVDVTLTTFNQ 609

DB 574 IRVRYAS-----TTNIRLSVNGSFGTISQNLPSMTMLRGDLRYGSFAIRENTSIRPTASP 629  
QY 610 SGVEIIIQ-NLSGYHLIVDKVFEIPIDIOIEKTKQCEGDICRCGVSQLETKKEIVNS 668  
DB 630 DQIRLTIEPSFIRQEVYVDRIEPIPVN-----PTR-----EAKEDLEAKKAVAS 674  
QY 669 LF 670  
DB 675 LF 676  
  
RESULT 11  
AEA81456  
ID AEA81456 standard; protein; 1156 AA.  
XX  
AC AEA81456;  
XX  
DT 25-AUG-2005 (first entry)  
XX  
DE *Bacillus thuringiensis* Cry9 protein, cry9a1, SEQ ID NO: 12.  
XX  
KW Transgenic plant; pesticide; genetically engineered microorganism; cry9;  
KW endotoxin.  
XX  
OS *Bacillus thuringiensis* serovar galleriae.  
XX  
PN US2005138685-A1.  
XX  
PD 23-JUN-2005.  
XX  
PF 21-DEC-2004; 2004US-00018615.  
XX  
PR 22-DEC-2003; 2003US-0531807P.  
XX  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
XX  
PI Flannagan RD, Abad AR;  
XX  
DR WPI; 2005-444221/45.  
XX  
PT New isolated nucleic acid encoding a polypeptide having pesticidal  
PT activity, useful for controlling pests, especially plant pests such as  
PT European corn borer, diamond-back moth or fall armyworm.  
PS Disclosure; SEQ ID NO 12; 114pp; English.  
XX  
CC The present invention relates to the *Bacillus thuringiensis* Cry9-family  
CC genes that encode delta-endotoxins having pesticidal activity against  
CC insect pests. The invention is useful for producing pesticidal  
CC compositions for controlling pests in plant such as European corn borer,  
CC diamond-back moth or fall armyworm. The invention is also useful in  
CC production of transgenic plant. The present sequence is the *Bacillus*  
CC *thuringiensis* Cry9 protein.  
XX  
SQ Sequence 1156 AA;  
  
Query Match 22.5%; Score 801.5; DB 9; Length 1156;  
Best Local Similarity 31.2%; Pred. No. 8.2e-65;  
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;  
  
QY 9 NTNEYILDGSPNNTMNSN---RYFPKDPNIPFNLDACQGRP---WQD-TWESVSDIV 61  
DB 2 NONKHGII-GASNCGCASDDVAKYPLANNPYSSALNLSQNSSLNINIIGDAAKEAV 60  
  
QY 62 TIGTVLIQFLLEPGIGG-IPVIFSIINKLI-PSSGOSVAALSICDLVSIIRKEVDESVL 119  
DB 61 SIGTTIVSLITAPSLTGLISIVDILGKVLGSSGQSISDLSICDLSSIILDRVSQSVLN 120  
  
QY 120 DGVADPEGEMTAYQDYLYLHLEDWLTDKSNPKKLA--DVVKQFOAREEDFTKLL----- 171  
DB 121 DGIADFNGLSVLLYRN-YLEALDSW---NKNPNSASAEELTRFRIADSEDFRILTRGSLT 176



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QY 172 -AGSLSRQKAEILLPTTVQAAHVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLK 230
Db 177 NGGSLARQNAQILLPLSPASAAFFHLLLRDARTRYGTWNG-----LYNATPPINYSKLV 231
QY 231 AKIKEYTNYCVGWYKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIPPTDYFEKY 290
Db 232 ELIELYTDYCVHWYKNGFNELRQGTSAWLEFHYRREMTLWLDIVASFSSLDITNY 291
QY 291 PLATSVELTREIYTPGVY----SGNYGWERFF---SPNSVEANGTRCPGLVTLQALD 343
Db 292 PIETDFQLSRVIYTPDPIGVHRSURGESWFSFVNRAFSDLE--NAIPNPRPSWFLNNMI 350
QY 344 IYSHSINILQGLSG----WGTRHYEDFTKNGAF--QRMSTGTTNNPRNIIFGNTDIF 397
Db 351 ISTGSLTLVPSPSTRARWYGSR--DRISPANSQFITEISGQHTTATQILGRN--IF 406
QY 398 KIISLARYAMQPFVGYISIPRHLVSRABFPPTT---LNTFLYE--VNSSGYS-----OTIES 448
Db 407 RVDSQACNLNDITYG-----VNRVAFVHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459
QY 449 VLPNGKDLPPSRWYSHRLSNA-----ACVQNETSRVNVFGWHTSMKKDNRIYPD 500
Db 460 YLPGENSID-PTPEDYTHLTTINLTGCLRQVANSRSSLVMYGMWTHKSLARNNTINPD 518
QY 501 KITQIPAVKAFALPAGTGVAGGYVTAGPGYTGDDVVTLPYQASLKIRLTSAPT--KNVR 558
Db 519 RITQIPLTKVDTRGTGVYV-----DPGFTGALLQRTDHSGLGVLRVQFPHLRQQR 573
QY 559 VRLRYASGGPGFRVERMSPSSVSNANFSRAT-----GGYSSFDYDVLTVTFNQ 609
Db 574 IRRVYAS---TTNIRLSVNGSFGTISQNLPSMTMLGEDLRYGSPAIRFNFTSIRPTASP 629
QY 610 SGVEILIQ-NLSGYHLIVDKVEFIPIDIQIEKTKQCEGDICRCGEVQSLETKKEIVNS 668
Db 630 DQIRLTIEPSIRQEVYVDRIEFIVN-----PTR-----EAKEDLEAAKAVAS 674
QY 669 LF 670
Db 675 LF 676

RESULT 12
AA82988
ID AA82988 standard; protein; 1279 AA.
XX
AC
XX
AC AA82988;
DT 12-SEP-2003 (revised)
DT 04-JUL-2000 (first entry)
XX
DE Native Cry9Aa toxin.
XX
XX Cry9Aa; insecticide; transgenic plants; pest control; crop protection.
XX
XX Bacillus thuringiensis; ssp. galleria.
XX
FH Key Location/Qualifiers
FT Misc-difference 8 /note= "Absent or unidentified amino acid"
FT Misc-difference 20 /note= "Absent or unidentified amino acid"
FT Misc-difference 35 /note= "Absent or unidentified amino acid"
FT Misc-difference 86 /note= "Absent or unidentified amino acid"
FT Misc-difference 95 /note= "Absent or unidentified amino acid"
FT Misc-difference 118 /note= "Absent or unidentified amino acid"
FT Misc-difference 118 /note= "Absent or unidentified amino acid"
XX
XX WO200011025-A1.
XX
XX 02-MAR-2000.

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XX 24-AUG-1999; 99WO-FI000698.
PF
XX 24-AUG-1998; 98FI-00001809.
PR
XX (UNIC-) UNICROP LTD.
PA
XX Kuwahinov V, Kanerva A, Koivu K, Pehu B;
PI
XX WPI; 2000-224660/19.
DR N-PSDB; AA293235.
XX
XX Modified synthetic DNA sequences comprise modification of the truncated
PT cry9Aa gene of Bacillus thuringiensis for improved insect control in
PT plants.
XX
XX Claim 1; Page 51-53; 90pp; English.
XX
XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
CC gene of Bacillus thuringiensis ssp. galleria can be used for the
CC production of a unique insecticidal protein having the same properties as
CC the N-terminal domain of the insecticidal protein encoded by the native
CC cry9Aa gene of Bacillus thuringiensis ssp. galleria. The insecticidal
CC toxin works by binding to specific receptor molecules in the gut of
CC insects with consequent formation of ion channels in the epithelium. This
CC action leads to ion efflux and paralysis of the intestinal function,
CC which causes death of the insect. The synthetic DNA sequences exhibit
CC enhanced expression through improved mRNA processing, stability, and/or
CC translation providing improved tolerance against target insects. They can
CC be used in the production of transgenic plants capable of expressing the
CC N-terminal domain of the insecticidal protein encoded by the native
CC cry9Aa gene. They therefore have a role in pest control and crop
CC protection. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 1279 AA;
Query Match 22.5%; Score 801.5; DB 3; Length 1279;
Best Local Similarity 31.2%; Pred. No. 9.8e-65;
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;
QY 9 NTNEYEILDGSPNNTNMSN---RYPFKADPNIFPINDACQGRP---WOD-TWESVSDIV 61
Db 130 NQKHGII-GASNCCGASDDVAKYPLANNPYPSALNLSQNSQILNWINIIGDAKEAV 188
QY 62 TIGTYLIQFLPEGIGG-IPVIFSIINKLI-PSSQGSVAALSICDIIVSIIRKEVDSVL 119
Db 189 SIGTTIVSLITAPSLTGLISIVYDLIGKVGSSGQISDLSICDLSIIDLRVSQSVLN 248
QY 120 DGVADFEGETAYQDYLYLHYLEDWLTDSNPKLA--DVVKQFQAREEDFTKLL----- 171
Db 249 DGIADFNGLVLLYRN-YLEALDSW---NKNPNASASAEELRFRADSEFDRILTRGSLT 304
QY 172 -AGSLSRQKAEILLPTTVQAAHVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLK 230
Db 305 NGGSLARQNAQILLPLSPASAAFFHLLLRDARTRYGTWNG-----LYNATPPINYSKLV 359
QY 231 AKIKEYTNYCVGWYKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIPPTDYFEKY 290
Db 360 ELIELYTDYCVHWYKNGFNELRQGTSAWLEFHYRREMTLWLDIVASFSSLDITNY 419
QY 291 PLATSVELTREIYTPGVY----SGNYGWERFF---SPNSVEANGTRCPGLVTLQALD 343
Db 420 PIETDFQLSRVIYTPDPIGVHRSURGESWFSFVNRAFSDLE--NAIPNPRPSWFLNNMI 478
QY 344 IYSHSINILQGLSG----WGTRHYEDFTKNGAF--QRMSTGTTNNPRNIIFGNTDIF 397
Db 479 ISTGSLTLVPSPSTRARWYGSR--DRISPANSQFITEISGQHTTATQILGRN--IF 534
QY 398 KIISLARYAMQPFVGYISIPRHLVSRABFPPTT---LNTFLYE--VNSSGYS-----OTIES 448
Db 535 RVDSQACNLNDITYG-----VNRVAFVHDASEGSRQSVYEGYIRTTGIDNPRVQNT 587
QY 449 VLPNGKDLPPSRWYSHRLSNA-----ACVQNETSRVNVFGWHTSMKKDNRIYPD 500

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Db 588 YLPGNSDI-PTPEDYTHLSTTINLTGGLRQVSNRRSSLMYGTWTHKSLARNNTNPD 646
Qy 501 KITQIPAVKAFALPAGTGVAGGVVITAGPGVTGDDVTLTPYQASLKLRLTSAPTN--KNYR 558
Db 647 RITQIPLTKVDRTRGVSVN-----DPGFIGALLQRTDHGSLGLVLRVQFPLHLRQOYR 701
Qy 559 VRLRYASGGPGPRVERMSPSSVSNANFSRPAT-----GGYSSFDYDVTLTFTNQ 609
Db 702 IIRVRYAS-----TTNRLSVNGSFGTISQNLPSMTMLRGEDLRYGSPFAIREFNTSIRPTASP 757
Qy 610 SGVEIIQ-NLGYHLIVDKVFPIDIOIEKTKQCFEGDICRCEGVOSLETKEIVNS 668
Db 758 DQIRLTIEPSIRQEVYVDRIEFIPVN-----PTR-----EAKEDLEAAKAVAS 802
Qy 669 LF 670
Db 803 LF 804

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## RESULT 13

AAV83039

ID AAV83039 standard; protein; 652 AA.

XX AC

AAV83039;

DT 04-JUL-2000 (first entry)

XX AC

Cry9Aa toxin N-terminal fragment.

DE DE

Cry9Aa; insecticide; transgenic plants; pest control; crop protection.

XX OS

Synthetic.  
Bacillus thuringiensis; ssp. galleria.

XX FH

Key Location/Qualifiers

XX FT

Misc-difference 650  
/note= "Position is either encoded by a stop codon or  
absent or unidentified amino acids"

XX FT

WO200011025-A1.

XX FN

XX PD

XX PD

XX PF

24-AUG-1999; 99WO-FI000698.

XX PR

24-AUG-1998; 98FI-00001809.

XX PA

(UNIC-) UNICROP LTD.

XX PI

Kuvshinov V, Kanerva A, Koivu K, Pehu E;

XX PI

WPI; 2000-224660/19.

XX DR

N-PSDB; AAZ93234.

XX PT

Modified synthetic DNA sequences comprise modification of the truncated  
Cry9Aa gene of *Bacillus thuringiensis* for improved insect control in  
plants.

XX PT

Disclosure; Fig 4; 90pp; English.

XX PS

Synthetic DNA sequences derived from the sequence of the truncated cry9Aa  
gene of *Bacillus thuringiensis* ssp. galleria can be used for the  
production of a unique insecticidal protein having the same properties as  
the N-terminal domain of the insecticidal protein encoded by the native  
cry9Aa gene of *Bacillus thuringiensis* ssp. galleria. The insecticidal  
toxin works by binding to specific receptor molecules in the gut of  
insects with consequent formation of ion channels in the epithelium. This  
action leads to ion efflux and paralysis of the intestinal function,  
which causes death of the insect. The synthetic DNA sequences exhibit  
enhanced expression through improved mRNA processing, stability, and/or  
translation providing improved tolerance against target insects. They can  
be used in the production of transgenic plants capable of expressing the

CC N-terminal domain of the insecticidal protein encoded by the native  
cry9Aa gene. They therefore have a role in pest control and crop  
protection  
XX Sequence 652 AA;  
SQ

Query Match 22.2%; Score 789.5; DB 3; Length 652;

Best Local Similarity 31.6%; Pred. No. 4.2e-64;

Matches 214; Conservative 130; Mismatches 243; Indels 91; Gaps 28;

Qy 18 GSPNNTNMN---RYPFADPNIPINLDACQGRP---WQD-TWESVDIVTIGTYLQF 70

Db 2 GMPNCCASDDVAKYPLANNPYSSALNLSNCONSSILNWINIIGDAAKEAVSIGTIVSL 61

Qy 71 LLEPGIGG-IPVIFSIINKLI-PSSGQVAALSTCDLVSIIIRKEDSVLSGDVADPEGE 128

Db 62 ITAPSLTGLISIVYDLIGKVLGGSGQISDLSICDLSIIDLRVSQSVLNDGADFNPS 121

Qy 129 MTAYQDYLYLHLEDWLTDKSNPKKLA--DVVKQFOAREEDFTKLL-----AGSLSRQK 179

Db 122 VLLYRN-YLEALDSW---NKNPNSASAEELRTFRITADSEFDRILTRGSLTNGSLARQN 177

Qy 180 ABILLPTYQAAVHLLLRDAVKYKXWGLVCPPLYPGSGRTDCNERLAKIKKEYTNY 239

Db 178 AQILLPSFASAAFPHLLLRDATRYGTNWG-----LYNATPFYNYQSKLVELIELYDY 232

Qy 240 CVGWTKGLDQIRQAGTSABVWSKFNKPREMTLAVLDIIAIPFYDYFEKYPLATSVLT 299

Db 233 CVHWYNRGFNELRQRCGTSATWLEFHRYRREMTLVLDIVASPSLDTNYPETDFQLS 292

Qy 300 RIYITDPVGY---SGNGYWERFF---SPNSVEANGTRCGPLVTLQADIDYSHSINLQ 352

Db 293 RVITYTDPIGFVHRSSLRGESWFSFVNANPFSDLLE-NAIPNPRPSWFLNNMIISTGSLTP 351

Qy 353 LGYLSG---WGTRHYEDFTKNGAF--QRMGTTNNPRNIIFGNTDIFKIISLARYA 406

Db 352 VSPSTDRARVMYGSR--DRISPANSQFITEILISQHTTATQTLGRN--IFRVDISOACNL 407

Qy 407 MQPFVGYISPRHLVSRAEFFPTT---LNTFLYE--VNSSGYS---QTISVLPKINKDL 457

Db 408 NDTTYG-----VNRAVFYHDASEGSRQSVYEGYIRTTGIDNPRVQNTIYLPGENSDI 460

Qy 458 PPSRTNYSRLSNA-----ACVQNETSRVNVFGVWTHSMKKDNRIYDPKTOIPAVK 509

Db 461 -PTPEDYTHLSTTINLTGGLRQVSNRRSSLMYGTWTHKSLARNNTINPDRIITQIPUTK 519

Qy 510 APALPAGTGYAGGYVTAGPGYTGDDVVTLTPYQASLKLRLTSAPTN--KNYRVLRYASGG 567

Db 520 VDRGTGTVSYVN-----DEGFIGALLQRTDHGSLGLVLRVQFPLHLRQYRIRVRYAS-- 572

Qy 568 PGPFPRVERMSPSSVSNANFSRPAT-----GGYSSFDYDVTLTFTNQSGVEIIQ- 617

Db 573 --TTNRLSVNGSFGTISQNLPSMTMLRGEDLRYGSPFAIREFNTSIRPTASPDQIRLTIEP 630

Qy 618 NLSGHLIVDKVEFIPID 635

Db 631 SFIRQEVYVDRIEFIPVN 648

## RESULT 14

AAV83040

ID AAV83040 standard; protein; 656 AA.

XX AC

AAV83040;

XX AC

04-JUL-2000 (first entry)

XX DE

Synthesised Cry9Aa toxin.

XX KW

Cry9Aa; insecticide; transgenic plants; pest control; crop protection.

XX OS

Synthetic.  
Bacillus thuringiensis; ssp. galleria.



PT for producing organisms with pesticide resistance.

XX  
PS Claim 12; SEQ ID NO 22; 178pp; English.

XX

This sequence represents an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

Sequence 671 AA;

Query Match 22.0%; Score 782.5; DB 8; Length 671;

Best Local Similarity 33.1%; Pred. No. 2e-63;

Matches 248; Conservative 111; Mismatches 221; Indels 169; Gaps 40;

QY 15 ILDGSPNNNTMSN---RYPFAKDPNIFPINLDACQGRPWQDTWES---VSDIVT----- 62

Db 1 MLDALRINSMNSCYPRYPYPLAKDPQMTMRNTNY---KEWLNMCDNTQFTGDISYSSPE 57

**Qy**      63 -----IGTVLIQLFLLEPGGIPVI--FSIINKLI-----PSSQGSAV 98  
              :  
              |||  
              :|||:

Db 58 AALSVRDAVLGTGINSVGTILSNL-----GVPLASQSGFIISRLTIGILWAGDPFEALM 110

99 ALSICDLVSIIRKEVDSEVLSDGVADFEGETAYQDYLLHYLEDWLTDKSNPKKLADVX 158

QY | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :

DB 111 VL----VBEIIKKSIDQVRENALRELEG-LQIGIMRLYQITRLQAMLVNKDNRRA-LVT 164

QY QFQAEEDFTKLAGLSLRKAEILTELPVQAANVHLLLEFDAYKYKEWGLVCPPLYP 210  
D6 QVAIVTNNSEETGMD-VKEEDNTHIIIDNYAQRNMVITLDDISCVQCOCI 212

219 GSERTDCNE---RIKAKTEVTNYCVGWYKGLDQIBOACTSAFVMSYKVKEDDEEMT AV 275  
105 QIAIADNFENAMF-NFNSKNFSLIDLLFVIAQAAANLHLLIIGKDAWIFGAWQL----- 211

217 --GDDTIRDNYIRLOGLREYKHCITFYNOGLNOENR--SNAODVSWENRFTDMLTAV 272

QY 276 LDIIFPTTYDFEKYPLATSVELTREIYTDPVGY-----SGG-NYGM--ERFSEFNSVEA 327

Db 273 L0LAILFNYDPRRYPLAVKTELREVVYTDVPGFTVLESGGRYPWYINPNTTFAMEN 332

QY 328 NGTRGPGLVTLQALDIYSHSINQLGYLSGWGCTRHYEDFTKNGAFQRMSCGTTNNP- 386

Db 333 NARRRPSYTWLNRIFVYRTRLGNMSDVRNIGGHTLVENGNDGSEITHNFGKDSITPI 392

QY 387 RNIIFGNTDIFKTIISLAPYAMQPVG-----YSIPRHLVSRAEFFPTTLN-----TFLYE 436

Db 393 QYFNFANLSVPSIESLARI---YLGTEANNYITSQYGSRVIFNTSINNVPGLRYE 448

QY 437 VNSSGYQSOTIESVLPGINKDLP-PSRTNYSHRLSNAACVQNETGR-----VNVFGW 486

Db 449 VPANLP SQTILSELPG--KDKPRPNAGDFSHRLS---YISNFDARRSSGGIVSLLTFGW 503

487 QY THISMKXONRIY PDKITOI PAVKAFALPAGTGYAG--GYVTAGPGYTGDDVWILPYQ-AS 543

DD	504	AHTSMDRNNRLEPKI QIDAVK-----GWCNIGIVPGP--TGGNLVXVSDSHS	553
OV	544	IKWIDI TGAPDTNKNVYVBI DVA ---SCCQCDQEDVDDSGDCCV	503
		GNANIGEDDA	502

543	MAKADJISOF INMIVIAKUKIA	-----	SOQFOFFIKVKNRSEFSSV	-----	SNMNIKSKFA	10G	393
544	IKVAKAPOROF--	SVYTRIPVACINTHGDATF	VHSGGSSHTVKNRSECNSS	-----	CPDSNNTI	1	509

594	YSSFDYVDYV-----LVTENOSGVEIIIIIONLSGVHLLVDKVEEPIPIDIOIEKCTK 643
Qy	

```

610 ESDEYIDVCGIFTPSINPLIRVQTQS-----FGTHAI-DKEFIPLN----- 651
Db

```

QY 644 CQFEGDICRCEGVQSLETKKEIVNSLFIN 672

Db 652 -TFPN-----QSLEKREQEVNDLFIN 671

Search completed: December 15, 2005, 10:14:38  
Job time : 201 secs

Result No.	Query			ID	Description
	Score	Match	Length		
1	1872	52.6	666	2	Q8VM62_BACTA
2	1610.5	45.3	666	2	Q7X3F7_BACTA
3	940.5	26.4	686	2	Q75Q05_BACTE
4	918.5	25.8	674	1	C24AA_BACTG
5	801.5	22.5	1156	1	CR3AA_BACTG
6	789.5	22.2	675	2	Q6BCH5_BACTU
7	773	21.7	1157	1	CR6AA_BACUK
8	772.5	21.7	1229	1	CR1BB_BACTU
9	772.5	21.7	1233	1	CR1BC_BACTM
10	756.5	21.3	719	1	CR1ID_BACTU
11	756	21.3	1228	1	CR1BA_BACTU
12	755	21.2	1228	2	Q93NM5_BACTU
13	754	21.2	1144	2	Q8KZL7_BACTE
14	754	21.2	1228	1	CR1BA_BACTE
15	754	21.2	1228	2	Q93T7E_BACTE
16	752.5	21.2	1160	1	CR8CA_BACTP
17	752.5	21.2	1228	2	Q62R6_BACTU
18	745.5	21.0	1231	2	Q8KNY2_BACTU
19	743.5	20.9	1231	1	CR1BD_BACTZ
20	731	20.6	675	1	C25AA_BACTJ
21	729	20.5	1169	1	CR8BA_BACUK
22	723.5	20.3	849	2	Q6FYW_BACTK
23	723.5	20.3	1227	1	CR1BE_BACTU
24	716	20.1	719	1	CR1IA_BACTK
25	716	20.1	719	2	Q6X181_BACTU
26	716	20.1	719	2	Q546K2_BACTK
27	716	20.1	746	2	Q4W4S8_BACTU
28	715	20.1	719	2	Q85796_BACTK
29	715	20.1	719	2	Q5SLW9_BACTU
30	714	20.1	720	2	Q4LDH4_BACTU
31	713	20.1	719	2	Q93NJ5_BACTU

Qy	5	NSVQNTNEYEILDGSPNNTMNSNRYPFKADPNIPFINLDACGRPWQDTWESVSDIVTTG	64
Db	1	NSYENKNYEYILSSSSNNTPNRYPPFANDRDMSTMFNDQCQISWEIWEESAETITSIG	60
Qy	65	TYLIOFLLEPGIGIPIVFSTINKLIPSSGGSVAALSICDLVSIIRKEVDESVLDPGVAD	124
Db	61	IDLIEPMEPSLGGINTLFSIIGKLIPTNHQSVSALSICDLVSIIRKEVADSVLSDAICR	120
Qy	125	F-EGEMTAYQDYIHLHLEDMLTD-----KSNPKKLADVVVQFOQAREEDFTKLLAGLSRQ	178
Db	121	FLDGKLKNYREYIPLYEAWLKDGCKPLQKTNNSDIGQLVKYFELSERDFNEILGGSLLRN	180
Qy	179	KAEILLPTVQAAVNHLLLLLRDVAVKYKKEW-----GLVCPPIYPQSG-----RTDCNR	228
Db	181	NAQILLIPYFCASCKQQLLLLRDAVQYEEWFFPLSAENVASELSPNSGCDFTGDYVER	240

QY 229 LKAKIKEYNYCVGNKGLDQIRAGTSAEWSKFNKFRREMTLAVLDIIAIFPTDYDFE 288  
 DB 241 LKCKIAEYTDYCEYVQAGLNOIKOAGTGADTWAKFNKFRREMTLTVLDIIAIFQTYDFK 300  
 QY 289 KYPLATSVELTREIYTDVPVYSGGNGWERFE--SFNSVEANGTRGPGIATWLQALDIYS 346  
 DB 301 KYPLATSVELTREIYTDVPVYSGGNGYVSMKYWTGAFNTLEANGTRGPGIATWLRSIGIYN 360  
 QY 347 HSINLQGLYSGWGGRHYEDFTKNGAFQRMSTNNPRNIIFGNTDIFKIIISLARYA 406  
 DB 361 EYVS---RYFSGWGTGRHYEDFTKNGAFQRMSTNNPRNIIFGNTDIFKIIISLARYA 414  
 QY 407 MQPFGV--YSIPRHLVSRAPFPTTLNFTLYEVNNGY-SQIESVPGINKDLPPSRTN 463  
 DB 415 IMNLVGEINARPEYVSRAPFPTTLNFTLYEVNNGY-SQIESVPGINKDLPPSRTN 473  
 QY 464 YSHRLSNAACVQNETSRVNVGWTHTSMKKNRIYDPDKITQIPAKAFALPAGTGVAGY 523  
 DB 474 YSHRLSNAACVQNETSRVNVGWTHTSMKKNRIYDPDKITQIPAKAFALPAGTGVAGY 530  
 QY 524 VTAGPGYGGDVVTLTPYQASLKIRLTSAPTNKNYRVRLYASGGPGPFRVERWSPSSVSN 583  
 DB 531 VIAGPGHTGNNVSLPYVSRKIRLIPASTNKNYRVRLYASGGPGPFRVERWSPSSVSN 590  
 QY 584 ANFSRATPGYSSPDYDVTLTFTFNQSGVEIIQNLSGVLHVDKVEFIPIDIEKCTK 643  
 DB 591 SYFFELPSTGPGSFGYDVTLTFTFNQSGVEIIQNLSGVLHVDKVEFIPIDIEKCTK 644  
 QY 644 COFEGDICRCGCVQSLEYKKEIVNSLFI 671  
 DB 645 LEYEGK-----QSLKRAQDVNDLVFV 665

RESULT 2

QYX3F7 BACTA  
 ID Q7X3F7\_BACTA PRELIMINARY; PRT; 666 AA.  
 AC Q7X3F7;  
 DT 01-OCT-2003 (TremBLrel. 25, Created)  
 DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
 DE Putative mosquitocidal toxin.  
 GN Name=cr40-like;  
 OS Bacillus thuringiensis (subsp. aizawai).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=1433;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Bun1-14;  
 RA Ito T., Sahara K., Amano S., Bando H.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB112346; BAC77648.1; -; Genomic DNA.  
 DR GO; GO:0006787; F:hydrolyase activity; IEA.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR GO; GO:0030435; P:sporulation; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin.C.  
 DR InterPro; IPR005639; endotoxin.N.  
 DR Pfam; PF03944; Endotoxin C; 1.  
 DR Pfam; PF00555; Endotoxin M; 1.  
 DR Pfam; PF03945; Endotoxin N; 1.  
 SQ SEQUENCE 666 AA; 75432 MW; F6E9E33309D06CDF CRC64;

Query Match 45.3%; Score 1610.5; DB 2; Length 666;  
 Best Local Similarity 50.6%; Pred. No. 2.6e-108;  
 Matches 356; Conservative 82; Mismatches 194; Indels 71; Gaps 20;  
 QY 4 MNSYQNTWEYELKDSPPNNTNSNRYPPAKDNIPINLDACGPRWQWTWESVDIVTI 63  
 DB 1 MNSYQNTWEYELKDSPPNNTNSNRYPPAKDNIPINLDACGPRWQWTWESVDIVTI 60

QY 64 GYLLIQFLLEPGIGGIPVIFSIINKLIPSSGQSVAAALSCDLVSIIRKEVDSVLSGVA 123  
 DB 61 GIDLITFLGPEISITGNLIFSIVIGLLP-SGQNVASLSICDLISIRKEVDSVLSDAY 119  
 QY 124 DPEGEMTAYQDYVYHLEDMITDKSNP---KKLADVVKQFOAREEDFTKLKAGSLRQKA 180  
 DB 120 DPNGVNNYQTYLLTSLKKWL-DAGKPTTGQLLTDVTHGFSEFSEFNFALLKSLSRPKG 178  
 QY 181 EILLPTTYQAAANVHLLLRDVAVKYKKEW-----GLVCPPLYPGSGRTDCNERL 229  
 DB 179 EILLPTTYQAGANLHLLLRDVAVKYKKEW-----GLVCPPLYPGSGRTDCNERL 231  
 QY 230 KAKIKEYNYCVGNKGLDQIRAGTSAEWSKFNKFRREMTLAVLDIIAIFPTDYDFE 289  
 DB 232 KEQLAEHINHCITWTYQAGLNQIKESGTSTENLKNKFRREMTLAVLDIIAIFPTDYDFE 291  
 QY 290 YPLATSVELTREIYTDVPVYSGGNGWERFE--SFNSVEANGTRGPGIATWLQALDIYS 347  
 DB 292 YKSETHIELSREVYTDVPVYN---GWEQNLNGENTLEANGTRGPGIATWLKIDIFTD 347  
 QY 348 SINLQGLY-----LSGWGGTRHYEDFTKNGAFQRMSTNNPRNIIFGNTDIFKIIISL 402  
 DB 348 EYVTSYSGSPVAILRGWAGTRHYEYTGSSNTLQIRISGTTSDVSNIDFINSRIFITSL 407  
 QY 403 ARYAM-----QPFVGYGSIPIRHLVSRAPFPTTLNFTLYEVNNGY-SQIESVLPFCINK 455  
 DB 408 ARYALAGAAAGNP-----GSPRYRVRVSRVPRSTGRYTFLYEVNNGY-SQIESVLPFCINK 463  
 QY 456 DLPPSRNTYSHRLSNAACVQNETSRVNVGWTHTSMKKNRIYDPDKITQIPAKAFALPA 515  
 DB 464 --ATGFTDYFNRLSNAACVQNETSRVNVGWTHTSMKKNRIYDPDKITQIPAKAFALPA 520  
 QY 516 GTGAGGYVGTAGPGYGGDVVTLTPYQASLKIRLTSAPTNKNYRVRLYASGGPGPFRVER 575  
 DB 521 GT-----SSVAGPGHTGNNVSLPYVSRKIRLIPASTNKNYRVRLYASGGPGPFRVER 575  
 QY 576 W--SPSSVSNANFS--RPATGG--YSSFDYDVTLTFTFNQSGVEIIQNLSGVLHVDKV 629  
 DB 576 WRGPGYVQEARHTVQRTFSGSMYDYSFKYLDIFTWPAEDYDFTDLTDLGSGGALYDKI 635  
 QY 630 EPIPIDIEKCTKQFEGDICRCGCVQSLEYKKEIVNSLFI 672  
 DB 636 EPIPDDL-----TTLLEYEE-----RNLEKTKNAVNDLFTN 666

RESULT 3

QY5Q05\_BACTE  
 ID Q75Q05\_BACTE PRELIMINARY; PRT; 686 AA.  
 AC Q75Q05;  
 DT 05-JUL-2004 (TremBLrel. 27, Created)  
 DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)  
 DE Putative mosquitocidal toxin.  
 GN Name=cr4Ba like;  
 OS Bacillus thuringiensis (subsp. entomocidus).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=1436;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=INA288;  
 RA Ikeya T., Yamaya K., Ito T., Sahara K., Bando H., Amano S.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=INA288;  
 RA Tomonori I., Kumiko Y., Takeshi I., Ken S., Shin-ichiro A.,  
 RA Hisanori B.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB161456; BAD08532.1; -; Genomic DNA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0005102; F:receptor binding; IEA.

DR GO:0006952; P:defense response; IEA.  
 DR GO:0009405; P:pathogenesis; IEA.  
 DR GO:0030435; P:sporulation; IEA.  
 DR InterPro: IPR001178; Endotoxin.  
 DR InterPro: IPR005638; Endotoxin\_C.  
 DR InterPro: IPR005639; Endotoxin\_N.  
 Pfam: PF03944; Endotoxin\_C; 1.  
 Pfam: PF00555; Endotoxin\_M; 1.  
 Pfam: PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 686 AA; 78023 MW; 1F0FD65618AE4D2 CRC64;

Query Match 26.4%; Score 940.5; DB 2; Length 686;  
 Best Local Similarity 34.3%; Pred. No. 1.7e-59;  
 Matches 252; Conservative 101; Mismatches 230; Indels 151; Gaps 26;

QY 4 MNSYQNTNEYELDGSPPNNTNMSNRYPPFAKDPNIPFIN-----LDACQ-----GRPWQD 52  
 DB 1 MNSYQNKNEYELNAPSNTNPNRYPPFANDPNAMKNGYKDWLDICNPEYRYSNP--E 58

QY 53 TWESVSDIVTIGTYLQFLLEPGIGIPV-----IFSINKLIPSS-----G 94  
 DB 59 AYRNTKAAMFCVGLVSTIL--GVLGGPISVTLGAIGVTVAVLEFIPADEYDNTKETWG 116

QY 95 QSVAAISICDLVSIIRKEVDESLSGVADFGEMTAYODYLHYLEDWLTDSKSNPKLA 154  
 DB 117 VLIAAIK-----ELIYEIKGEAMNAKALDGLYKVMKNYD-NKLNVMKNGDKSPVEQN 170

QY 155 DVVKQFQAREEDFTKLAGLSRQAEILLPTTYVQAANVHLLLRDAVYKKEGLVCP 214  
 DB 171 EIQRVFAFDNTNSFL--LLISQFOQLGHEVSFLFPAFAANFHLRLDVSIVYKGGYNT-N 228

QY 215 PLYPG--SGRTDCNERLAKIKEYTNYCVGWKGLDQIRQAGTSAEV--WSKFNFRFRM 271  
 DB 229 NIEGYHSDQDMTO-----DYTYAVDTNKGLEEAANKIKNKDLQWDFYQVRRDM 281

QY 272 TLAVLDIIAIFTYDFEKYPLATSVELTREIYTDVGY-----SGNGYWERFES 321  
 DB 282 TLTVLDVIALFTYDVRKYPISTKVELTREIYTDMINYNNPMTNPFVGGQFAGYTAQ 341

QY 322 FNSVEANGTRGPGVLTWLAQDIYSHSINLQGLYSGWGTRH---YEDFT-KGNAFOR 377  
 DB 342 FNSIENALTREPHLFTLKEVTGYFAQYQQQSFMTGIGNTSYRTNYEDYPPSGPLHGV 401

QY 378 MSGTSSNNPRTIIFGNTDIFKILSLARYAMQPFVGYSPRHLVSRAPPTTLNLTFLYEV 437  
 DB 402 YAGDTA---RSVDNNGKDVSIYS-----TMPPLETNNHVEL 436

QY 438 -----NSS-----GYSQTIISVLPINKD--- 456  
 DB 437 RPTATYFVGKGRHDATDRRTGNSSQKLGEDSKTGRTATGPSYFI-SEIYYDKETNE 495

QY 457 -LPPSRNTYSHRLSNAACVQNETSRV-----VFGWTHTSMKKNRIYDPDKIT 503  
 DB 496 TIRTPPEKNHRLSVISAYATDCGRISGVRGDCFRTPQMCATWHSADPYNTIHPDKIT 555

QY 504 QIPAKAFALPAGTYAGGYVTAGGYTGGDVVTLPYQASLKIRLTSAPTNKYVRLEY 563  
 DB 556 QISAVKAFYI-WDQT--EGQVSGPGFTGGDLVLPYNARLKIRLKPSTSTSKYVRVRY 612

QY 564 ASGGPGPRVERWSPSSVSNANFSRPATGG---YSSFDVDTLVTTENOSGVETIIQNL 620  
 DB 613 ASMGAGTURAESKWSPYGVSFNSFAYEYTGDSNKFNNFKYLETLSSEFNSIGVEIIQNL 672

QY 621 GYHLIVDKVERFIPI 634  
 DB 673 SSQQLIVDKLEFIPI 686

RESULT 4  
 C24AA BACTJ STANDARD; PRT; 674 AA.  
 AC O87905;  
 DT 16-Oct-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Pesticidal crystal protein cry24Aa (Insecticidal delta-endotoxin  
 DE CryXIVA(a)) (Crystalline entomocidal protoxin) (Crystal protein)  
 DE (Insecticidal protein Jcg72) (Fragment).  
 GN Name=cry24Aa; Synonyms=cryXXIVA(a);  
 OS Bacillus thuringiensis subsp. jegathesan.  
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=56955;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RA Kawalek M.D., Gill S.S.;  
 RP "Isolation and characterization of insecticidal genes from Bacillus  
 RT thuringiensis subsp. jegathesan.";  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
 CC epithelial cells of insects.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL: U88188; AAC61891.1; -; Genomic\_DNA.  
 DR HSP; Q06117; LJI6.  
 DR InterPro: IPR001178; Endotoxin.  
 DR InterPro: IPR005638; Endotoxin\_C.  
 DR InterPro: IPR005639; Endotoxin\_N.  
 DR Pfam: PF03944; Endotoxin\_C; 1.  
 DR Pfam: PF00555; Endotoxin\_M; 1.  
 DR Pfam: PF03945; Endotoxin\_N; 1.  
 DR Sporulation; Toxin.  
 KW NON\_TER 674 674  
 FT  
 SQ SEQUENCE 674 AA; 75959 MW; DA3904DAB891C978 CRC64;

Query Match 25.8%; Score 918.5; DB 1; Length 674;  
 Best Local Similarity 33.2%; Pred. No. 6.6e-58;  
 Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY 4 MNSYQNTNEYELDGSPPNNTNMSNRYPPFAKDPNIPFIN-----LDACQGRPWQDTWESV 57  
 DB 1 MNSYQNKNEYELLESQNNMNPRIYPPADDPNAVMMKNGYKDWVNECEG-----SNISP 55

QY 58 SDIVTIGTYLQFLLEPGIGIPVIFSINKLIPSSG-----QSVAAISICDLVSIIR 110  
 DB 56 SPAAITSKIVSIVLTKLAKA--VASSLADSIKSSLSGSKITENNVSQVSMVQVHQIIN 113

QY 111 KEVDESLSGVADFGEMTAYODYLHYLEDWLTDSKSNPKLADVVKQFQAREEDFTKL 170  
 DB 114 RRIQETILDGSSSLNGLVAIYNRDYLGALEANNKNSINITYQTNVAEAFKTYVEREFTK 173

QY 171 LAGLSRQKAEILLPTTYVQAANVHLLLRDAVYKKEGLVCPPLYPGSGRTDCNERLK 230  
 DB 174 LKGIYRTSSSQITLPTTQAANVHLLSMURDAVMYQEGWNL-----QSHINYSKELD 225

QY 231 AKIKEYTNYCVGWKGLDQIRQAGTSAEVSKFNKFRREMTLAVLDIIAIFTYDFEKY 290  
 DB 226 DALEDYTNVCVEYTKGLNALR--GSTAIDWLEFNSFRDMLVLDLVAIFPNYPRVY 283

QY 291 PLATSVELTREIYTDVPGVSGG-NYG-W-----ERFSSFNSEANGTRGPGVLTWLAQDI 344  
 DB 284 PLSTKISLSRKIYTDVGRDTSFSGDWTNTGTLANFNDLREVEVTDSPSLVKWLGDMTI 343

QY 345 YSHSINLQGLYSG-----WGTTHYEDFTKNGAFQMSGTSSNPNRIIFGN---TD 395

Db 344 YTGAIIDSVRPTSPGDRIGVWYGNINAFVHTGRTDVMFRQGTDTAYEDPSTFISNLYDD 403  
 QY 396 IFKI-----ISLARYANQPPFVGYSIPRHLVSRAEFFFTTLNTFLYEVNSGYSQTISV 449  
 Db 404 IYKLDLRAAAVSTIQAMDITFG-----VSSRFDFIRGNQLYQSNKPYPSLPITIT 456  
 QY 450 LPGINKDLPPSKRTNYSRHLNAAVCQNETSrv-----NVFGWTHSMKKDNRIYDPKI 502  
 Db 457 FPG-EESEGNANDVSHLLCDVKIIQEDSSNICGRSSLLSHAWTHASLDNRNTLLPDEI 515  
 QY 503 TQIPAVKAFALPAGTGYAGGYTAGGYTGGDVVTLPYQA--SLKIRLTSAPTNKYRVR 560  
 Db 516 TQIPAVTAYELRGNSS-----VVGPGSTGGDLVWMSYHVSFKVYCSL---KNYRVR 567  
 QY 561 LRYASGGPGPRVERWSSVSNANFSRATGG-----YSSFDYVDTLVTFNQSGVE 613  
 Db 568 IRYASHGNCQFLMKRWPSGTGVAQRWHRNVQGTFSNMRVEAFKYLDITFTTPEENFA 627  
 QY 614 IIQNLSCYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCGVQSLETKEIVNSLFIN 672  
 Db 628 FTIDLESGDLFIDKIEFIPV-----SGSAFEYEGKQNIETQKAVNDLFIN 674

## RESULT 5

## CR9AA BACTG

ID CR9AA BACTG STANDARD; PRT; 1156 AA.  
 AC Q99031; Q03747;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Peatidial crystal protein cry9Aa precursor (insecticidal delta-  
 DE endotoxin CryIXa(a)) (Crystalline entomocidal protoxin) (130 kDa  
 DE crystal protein).  
 GN Name=cry9Aa; Synonyms=cryIG, cryIVA(a);  
 OS Bacillus thuringiensis subsp. Galleriae;  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_taxid=29338;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 24-34.  
 RC STRAIN=11-67;  
 RX MEDLINE=92070568; PubMed=1660003; DOI=10.1016/0014-5793(91)81144-W;  
 RA Smulevitch S.V., Osterman A.L., Shevelev A.B., Kaluger S.V.,  
 RA Karasin A.I., Kadyrov R.M., Zagnicko O.P., Chestukhina G.G.,  
 RA Stepanov V.M.;  
 RT "Nucleotide sequence of a novel delta-endotoxin gene cryIG of Bacillus  
 RT thuringiensis ssp. galleriae.";  
 RL FEBS Lett. 293:25-28(1991).  
 RN [2]

## NUCLEOTIDE SEQUENCE OF 1-1151.

RC STRAIN=DSIR517;  
 RX MEDLINE=92211329; PubMed=1556556;  
 RA Gleave A.P., Hedges R.J., Broadwell A.H.;  
 RT "Identification of an insecticidal crystal protein from Bacillus  
 RT thuringiensis DSIR517 with significant sequence differences from  
 RT previously described toxins.";  
 RL J. Gen. Microbiol. 138:55-62(1992).  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of insects. This protein is toxic to Galleria  
 CC mellonella.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

DR EMBL; X58120; CAA41122.1; -; Genomic DNA.  
 DR EMBL; X58534; CAA41425.1; -; Genomic DNA.  
 DR PIR; S19306; S19306.  
 DR HSP; P02965; ICY1.  
 DR InterPro; IPR003305; Cenc carb bd.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR005639; endotoxin N.  
 DR Pfam; PF02018; CEM\_4\_9; 1.  
 DR Pfam; PF03944; Endotoxin C; 1.  
 DR Pfam; PF00555; Endotoxin M; 1.  
 DR Pfam; PF03945; Endotoxin N; 1.  
 KW Direct protein sequencing; Sporulation; Toxin.  
 FT PROPEP 1 23 Removed in mature form.  
 FT CHAIN 24 1156 Peatidial crystal protein cry9Aa.  
 SQ SEQUENCE 1156 AA; 129727 MW; 785F65B1B1165FF2 CRC64;  
 Query Match 22.5%; Score 801.5; DB 1; Length 1156;  
 Best Local Similarity 31.2%; Pred. No. 4.8e-49;  
 Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;  
 QY 9 NTNEYIILDGSPNNTMSN---RYPPAKDPNIFPINLDACQGRP---WQD-TWESVSDIV 61  
 Db 2 NQKHGII-GASNCGCASDDVAKYPLANNPYSSALNLSQNSQILNWINIIGDAAKEAV 60  
 QY 62 TIGTYLIQFLLEPGIGG-IPVIFSIINKLI-PSSQSVAAALISICDLVSIIRKEVDESVL 119  
 Db 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGGSSQGISDLISICDLISIDLRVSQSVLN 120  
 QY 120 DQVADPEGETAYQDYLYHLEDLWLTDKSNPKLA-DVVQFOAREEDFTKLL----- 171  
 Db 121 DGIADFNGSVLLYRN-YLEALDSW---NKNPNSASABELRFRTRFADSEFDRILTRGSLT 176  
 QY 172 -AGSLSRQKAEILLPTVQVQANVHLLLRDAVKYKKEWGLVCPPLPGSGRTDCNERLK 230  
 Db 177 NGGSLARQNAQILLPSPASAAFFHLLLRDATRYGTNWG-----LYNATPPINYOQSLV 231  
 QY 231 AKIKSYTYCVGWYKNGLDQIRQAGTSABVSKFNKPREMTLAVLDIIAIPPTYFEKY 290  
 Db 232 ELIELYTDYCVHWYNRGFEFLRQRTSATATWLEFHYRREMTLWVLVDIVASFSSLDITNY 291  
 QY 291 PLATSVELTREIYTDVPGY-----SGNGYWERFF---SENSVEANGTRGGLVTLWLAID 343  
 Db 292 PIETDFQLSRVIYTDPIGFVHRSSLRGSEWFSFVNANFSDLLE-NAIPNRPSPFWLNNMI 350  
 QY 344 IYSHINILQGLYLSG---WGTRHYEDFTKNGAF--QRMSGTTSSNNPRNIFGNTDIF 397  
 Db 351 ISTGSLTLFVSPSTDRARWYGSR--DRISPANSQFITEISGOHTATQTILGRN--IF 406  
 QY 398 KIISLARYAMQPFVGYISIPRHLVSRABFPPTT---INTFLYE--VNSSGYS-----QTIES 448  
 Db 407 RVDSQACNLNDTTYG-----VNRVAFYHDASEGSRQSVYEGYIRTTGIDNPRVQNI 459  
 QY 449 VLPGLINKDLPPSRTHYSHRLSNA-----ACVQNETSRVNVFGWTHTHSMKKDNRIY 500  
 Db 460 YLPGENSDDI-PTPEDYTHLSTINLTGGLRQVAGSNRRSSLVMYGTWHTSKLAANNINPD 518  
 QY 501 KITQIPAVKAFALPAGTGYAGGYTAGGYTGGDVVTLPYQASLKLRLTSAPTNN--KNYR 558  
 Db 519 RITQIPLTQVTRGTGVSYN-----DPGFIGALLQRTDGHSLGLVLRVQFPHLRQOYR 573  
 QY 559 VRLRYASGGPGPRVERWSSVSNANFSRAT-----GGYSSFDYVDTLVTFNQ 609  
 Db 574 IRRVYAS---FTNIRLSVNGSFGTISQNLPSLTMRLGEDLRYGSPFAIREFNTSIRPTASP 629  
 QY 610 SGVEIIIQ-NLSGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCGVQSLETKEIVNS 668  
 Db 630 DQIRITIEPSFIRQYVYVDRIEFIPVN-----PTR-----BAKEDLEAAKKAVAS 674  
 QY 669 LF 670  
 Db 675 LF 676



```

RESULT 6
Q6BCH5 BACTU PRELIMINARY; PRT; 675 AA.
ID Q6BCH5
AC Q6BCH5
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Delta-endotoxin.
GN Name=cry24-like;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=96-OK-85-24;
RA Ohgushi A., Saitoh H., Wasano N., Ohba M.;
RT "Cloning and characterization of novel cry genes from a mosquitoicidal
RT Bacillus thuringiensis serovar sotto strain."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB185105; BAD32657.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF03945; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
SQ SEQUENCE 675 AA; 75906 MW; E983D92F9053AEE8 CRC64;

Query Match 22.2%; Score 789.5; DB 2; Length 675;
Best Local Similarity 32.1%; Pred. No. 1.6e-48;
Matches 235; Conservative 106; Mismatches 270; Indels 121; Gaps 27;

QY 4 MNSYQNTWEYELDQSPNNTMSNRYPPAKDNPFPIN-----LDACOG-----RPQD 52
DB 2 VNPYQKSESVFYHSHNQKQIDPNRYPTNPNNAVMKNGYKDWNECEGSNVSPSPAA 61
QY 53 TWESVSDIV--TIGYLIQFLLEPGIGGIPVIFSIINKLIPSSGOSVAALSICDLVSIIR 110
DB 62 VTSALISIVLTKALVSSLVD-AIKSLGISEVITK-----NNVSLSMELVNLIN 114
QY 111 KEVDESVLSDGVADPEGEMTAYQDYLYHLEDWLTDKSNPKKLADVVKQFQAREEDFTKL 170
DB 115 RRIQETINDLSASLNGLSYK-RYLALEAWDKSNITLQENVIEEFKVESRFFEN 173
QY 171 LAGLSRQKAETILLPTVQAAVHLLLRDAVYKKBGLVCPPLPGSGRTDCNERLK 230
DB 174 LKGIYRTSSSQITLLPTFAQAANLHLSMLRDAVMYQEGWNL-----QSHLDYKMWLD 225
QY 231 AKIKEYTNYCVGWYKGLDQIRQAGTSAEVWSKFNKPREMTLAVLDLIAIPTTDFEYK 290
DB 226 IALDKYTNVCEVYVNRGNLALR--GSTALDMLFNSFRDMTLMVLDLVAIFPNYDPVQY 283
QY 291 PLATSVELTREIYTPDVGYSG---GNYGW---ERFFSFSVEANGTRGCLVTLWLOAI 342
DB 284 PLPTKIGLSRKLYTDPVGTTRDTDFGN--WLTDLTLANFDLDRDVTDSPLVKWLDVM 341
QY 343 DIYSHSINLQGY-LSGNGGTR-----HYEDF--TKNGAFQRMGTTNNPNRIIFGN 393
DB 342 NIYTGAI--SYPISGPGRIGVWYGNMNSFVLTSRSLSYNMYGEIAHEDPITNIRD 398
QY 394 TDIFKI-----ISLARVAMPQFVGYSPRLHLSRAEFPPTLTFLYEVNSSGVSQIE 447
DB 399 NDIYKVDLRAAYATIRNALDSTFG-----VSSSHFFNVGMKNELYSQKQYPSYPT 451
QY 448 SVLPGINKDLPPSRNTYSHRLSNAACVQNETSRVNVFG-----WHTSMKKDNRIYP 499

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## RESULT 7

```

CR8AA BACUK
ID CR8AA BACUK STANDARD; PRT; 1157 AA.
AC Q45704;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cry8Aa (Insecticidal delta-endotoxin
DE CryVIIIa(a)) (Crystalline entomocidal protoxin) (131 kDa crystal
DE protein).
GN Name=cry8Aa; Synonyms=cryVIIIa(a);
OS Bacillus thuringiensis subsp. kumamotoensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=132267;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=NRRL B-18746 / PS50C;
RA Payne J.M., Sick A.J., Foncarrada L.;
RT "Novel coleopteran-active Bacillus thuringiensis isolate and a novel
RT gene encoding a coleopteran-active toxin."
RL Patent number EP0498537, 12-AUG-1992.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U04364; AAA21117.1; -; Genomic DNA.
CC HSSP; P07130; 1DLG.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC Pfam; PF03944; Endotoxin C; 1.
CC Pfam; PF00555; Endotoxin M; 1.
CC Pfam; PF03945; Endotoxin N; 1.
CC Sporulation; Toxin.
CC KW
CC SEQUENCE 1157 AA; 131010 MW; 687B5C49DE93683B CRC64;

Query Match 21.7%; Score 773; DB 1; Length 1157;
Best Local Similarity 30.5%; Pred. No. 5.7e-47;
Matches 224; Conservative 126; Mismatches 265; Indels 120; Gaps 31;

QY 6 SYQNTNEYILDGSPNN--TNMSNRYPPAKDNPFPINLDACQGRPKQD-----TWESVS 58

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Db 2 SPNNQNEYEIADPTSTSVSSDSNRYPFANEPT-----DALONNNYKDYLMKSGGENPE 55  
 Qy 59 DIVTIGYLYQLFLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAALSI 102  
 Db 56 LFGNPETFISSSTTQTGIGIVGRIGALGVPFASQIASFYFIVGQLWPSKSVDIWGEIM 115  
 Qy 103 CDLVSIIRKEVDESVLSDGVADFEGETAYQDYLYLHLEDMWLTOKSNPKLADVVVKQFOA 162  
 Db 116 ERVEELVDQIEKVYKDKALAEKGLGNAL-DVYQOSLEDWLENRDARTSVSNQPIA 174  
 Qy 163 REEDFTKLLAGLSRQKAEIILLPTTYQAAVNHLLLRDAVKYKKEGLVCPPIYPGSGR 222  
 Db 175 LDLSNFVSIP-SPAVSGHEVLLAVYAQAVNLHLLLRDASIFGEWGT-----PGEIS 228  
 Qy 223 TDCNERLKAKIKETNYCVGHYKNGLDIOIRAGQSAEVSFKFPERREMTLAVLDITAI 282  
 Db 229 RFYNRQVL-TAEYSYDCVKRYKGLDKL-GTTSKSLNLYHQFRREMTLLVLDLVALF 285  
 Qy 283 PTYDFEYKPLATSVELTREIYTDVGVY-----SGNGYQWERF--FSFNSVEANGTRGPGL 335  
 Db 286 PNVDTHYPIETTAQLTRDVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVPHPH 345  
 Qy 336 VTWLQAIIDYSHSINLQ-----GYLSGMGG-TRHYEDEFKNGAFQRMSTGTTNNPRNIIF 391  
 Db 346 FDIILSSVEINTSRGGITLNDAYINYSGHYTLKRRRTADSTVYTYTANYGRITSEKNSPAL 405  
 Qy 392 GNTDIFKILS-----LARYAMQPFVGYISIPR--HLVSRAEFPPTTLNFTLFEVNSS---G 441  
 Db 406 EDRDIFINSTVANLANYQK---AYGVPGSWFHMKRG---TSSTTAYLSKTHALQ 459  
 Qy 442 YSOTIESVLPICGINKDLPSPRT-----NYSHRLSNAACVQNETSRVN-----VCGWT 487  
 Db 460 CTQVYES-----SDEIPLDRTVPVAESYSHRLSH---ITSFSKNGSAYVGSPPVFWMT 511  
 Qy 488 HTSMKKDNRIYDPKITQIPAVKAFALPAGTCYAGGYTAGPGYTGDDVW--TLPYQASLK 545  
 Db 512 HTSADLANNTIYSDKITQIPAVKGMWL-----YLGSSVVGPGFTGGDILKTNPSILGTF 566  
 Qy 546 IRLTSAPTKNRYVRLRYASGGPGPFRVERWSPSSVSNANFSRATGG-----YSSFDVVD 601  
 Db 567 AVTVNGSILSQRVRIIRYAS--TTDFEFTLYGDTIEKNRKNKTMGNGASLTYYETFKPAS 624  
 Qy 602 TLVT-TNQSGVEIILQN---LSGHLIVDKVEPIPIDIOIEKTKCOFEGDICEGVO 657  
 Db 625 FITDFQRETQDKILLSGDFSGOEYVIDRIEFIPVDY-----EBAQ 669  
 Qy 658 SLETKKEIVNSLFIN 672  
 Db 670 DLEAAKAVNALFTN 684

## RESULT 8

CR1BB BACTU STANDARD; PRT; 1229 AA.  
 AC Q45732;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 13-SEP-2005 (Rel. 46, Last annotation update)  
 DE Pesticidal crystal protein cryIb (Insecticidal delta-endotoxin  
 DE CryIb(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN Name=cryIb; Synonyms=cryE15, cryIb(b);  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=NRRL B-21110 / EG5847;  
 RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;  
 RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins  
 RT toxic to lepidopteran insects."  
 RL Patent number US5322687, 21-JUN-1994.  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut

CC epithelial cells of many lepidopteran larvae.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; L32020; AAA22344.1; -; Genomic\_DNA.  
 DR HSP; P02965; ICY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005639; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 1229 AA; 139771 MW; A4C949DB675C3269 CRC64;  
 Query Match 21.7%; Score 772.5; DB 1; Length 1229;  
 Best Local Similarity 32.1%; Pred. No. 6.7e-47;  
 Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;  
 Qy 11 NEYEILD--GSPNNNTMSNRYPPFAKDPNIFPI-----NLDACQCRPQDWTWESYDIV 61  
 Db 7 NENEIINALSIPTVSNPSTQNLSPDARIESLCVAEVNID-----PFVSA-STVQTGI 60  
 Qy 62 TIGTYILQFLEPGIGIPVIFS-IINKLIPSSGQSAALSICDLVSIIRKEVDESVLSD 120  
 Db 61 NIAGRILGVGPAGQLASFVFLVGLWP-SGRDPWEIPLHEVQLIRQOVTEINTRT 119  
 Qy 121 GVADFEGETAYQDYLYLHLEDMWLTOKSNPKLADVVVKQFOAREEDFTKLLAGLSR-OK 179  
 Db 120 AIARLEGIGRYSYQ-QALETLNDRNDRSILERYVALELDITAI--PLFIRN 176  
 Qy 180 AEIILLPTVQAAVNHLLLRDAVKYKKEGLVCPPLYPGSGRTDCNERLKAKIK--EV 236  
 Db 177 EEVPLMVAQAANLHLLLRDASLFGSEWG-----ASSDVNYQYQIRTEY 227  
 Qy 237 TNYCVGWYKGLDQIRAGTSAEVSFKFPERREMTLAVLDIILPTTYDFEYKPLATSV 296  
 Db 228 SNHCQVWYNTGLNNLR--GTNAESWLYNQPRDLTLGLVLDLVALFPSYDTRTPINTSA 285  
 Qy 297 ELTREIYTDVPGYSGNGYVW--ERPF-----SFNSVEANGTRGPGLVTLQALDIYSHSI 349  
 Db 286 QLTREIYTDPIGRTNAPSGFASTNWNFNNAFSAIEAIFRPPHLLDFPEQLTIYSAS- 344  
 Qy 350 NLQLGLSGMGTRHYEDFTKNGAFQRMSTG-----TSNNPRNIFGNVDIFK 398  
 Db 345 -----SRWSSQHMNYVWGHRLNFRPIGGTLNTSTQGLTNWTSINPTVLTQFTSRDVR 397  
 Qy 399 IISLARYAMQPFVGYISIRHLVSRAEF-FPTTLNFTLFEVNSGQSQTIESVLPGI---- 453  
 Db 398 TESNA-----GTNILFTTPVNGVPWAFNFINQN--IYERGATTYSQPYQGV--GLQLFD 449  
 Qy 454 -NKDLPSPRT-----NYSHRLSNAACVQNETSRVNFGWTHSTMKONRIYDPDKITQIP 506  
 Db 450 SETELPPTETTERPNYESYSHRLSHGLIIGTLRAPVYSWTHRSADRNTTIGPNRITQIP 509  
 Qy 507 AVKAPALPAGTCYAGGYTAGPGYTGDDVVTLPYQASL-KIRLT-SAPTKNRYVRLRYA 564  
 Db 510 LVKALNL-----HSGVTVVGPGFTGGDILRNTGTGFDIRNLINPLVSQRVRIIRA 564  
 Qy 565 SGGPFPFRVERWSPSSVSNANFSRATGG-----YSSFDYVDVTLVTFN---QSGVEIIL 616  
 Db 565 STTDQLQ-FTRINGITVAIGNFSRTMRGNDNLEYSFRATG-FSTPFNFNAQSTFLGA 622



```
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match      21.3%; Score 756.5; DB 1; Length 719;
Best Local Similarity 31.9%; Pred. No. 4.6e-46;
Matches 224; Conservative 118; Mismatches 23; Indels 121; Gaps 32;

Qy 2 KNMSYQNTNEYILDGSG-----PNNTNM-----SNRYPPFAKDPNIFPINLDACQGRPWQD 52
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 53 TWESVSDIVTGTVLIQLELPEGIG-----GIPV-----IFS-IINKLIPSSQGS 96
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 47 EYESVEPEFVSST-----IQTGIGIAGKILGNLGVPPAGVVASLYSIFLIGELWP-KGKS 99
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 97 VAALSICDLVSIIRKEVDESVLSDGVADPEGEMTAYQDYLYLHYLEDWLTDKSNPKKLADV 156
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 100 QWEIFMEHVEELINQKISTYARNKALADKGLGDALAVIH-ESLESWIENRNNTKRVSV 158
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 157 VKQFAEEDFTKLIALGSLRQKAEILLPTVQAANVHLLLRDAVKYKKEWGLVCPPL 216
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 159 KNQYIALELMFVQKLP-SFVSGSEVPLPIYAQAANLHLLLRDASIFGKEWGL----- 212
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 217 YPGSGRTDCNRLKAKIKEYTNYCVGYNKGLDQIRQAGTSAEVWSKFNKFRREMTLAVL 276
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 213 -SESEISTFYNNKSSQTSQYSDYCEWNTGLNRLR--GTNAESWVRYNQFRDRDMLMVL 269
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 277 DIIAIFPYDEKYPPLATSVBELTRIYIDPVG--YSGGNYGWERFF-----SFNSVEANG 329
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 270 DLVALFPSTYTRMYPPIPTSAQLTREVTYDAIGTVHPNAPSPASTTWNYNNAFSPFTIEAAV 329
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 330 TRGELVTWLOAIDY----SHSINQLGLVSGCGTGHVEDFTKNGAFAQ---RMSGTTS 383
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 330 VRNPHLLDFEQVIYISLLRSWNTQ--YNNMGG--HKLEFRTIGGTLNTSTQSGTWTIS 385
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 384 NNPRNIIFGNTDIFKIISLA---RYAMQPFVGYISIPRHLVRAEP-----PPTLTNLTFL 434
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 386 INPVTLPSTRDVRVSTESLAGLNFLTPQVNG-----VPRVDPHMKFVTHPIASDNFY 438
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 435 YEVSNGSYQIESVLPINKDLPSRT-----NYSHRLNNAACVQNETSRVNVFGWTH 488
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 439 Y----PGYA-GIGTQLQDSNELPEPTTGPQPNYESYSHRLSHIGHISASHKALVYSWTH 493
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 489 TSMKKNRIYDPKTIQIPAVKAFALPAGTGVAGGVVTVAGPGVTGGDVVTLPYQASL-KIR 547
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 494 RSADRTWINDSITQIPLVKAFNLPASGAS-----VVRGPGFTGGDIILQRTNTGTFGDIR 548
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 548 LT-SAPTNNKYRVLRYASGGPGPRVBRWSPSSVSNANFRPATGG-----YSSPDYVD 602
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 549 VNINPPFAQYRLRYASTTNLEPHTS-INGKAINQGNFSATMNRGEDLDYKAFRTVG- 606
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 603 LVTFN-----QSGVEIILNLS-GVHLIVDKVEFIPIDIQIE 639
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 607 FTTTPFSNAQSTFTIGAWNFSLGNEVDYIDRIEFVPEVTYE 648
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
ID CRIBA_BACTK STANDARD; PRT; 1228 AA.
AC POA373; P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 46, Last annotation update)
DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin
GN CryIIa(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
DN Name=cryIIa; Synonyms=cryA4, cryIIb(a);
OS Bacillus thuringiensis subsp. kurstaki.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCB1_TaxID=29339;
```

287 YTDAGATGVNMASNMVNNNAPSFSAIEAAIRSPHLLDFLEQITIFSAS-----S 338  
358 GWGCTRHYEDFTKGNGAFQMSG-----TTSNNRNIIIEGNTDIFKIIISLARVA 406  
339 RWSNTRW-TWRGRTTQSRPIGGGLNTSTHGATNTSINPVLTRFASRDVYTESVAGVL 397  
407 MQPFVGYGISPRHLVSRAEF-EFTTLNTFLYEVNSSGYQTIESVLPGI-----NKDLPES 460  
398 LWGI--YLEPIHGVPTRFNTFNQN--ISDRGTANYSQPYES--PGLQLKDSLETLPPE 451  
461 RT-----NYSHRLSNACVQNETSRVNVFGWTHTSMKKONRIYDPKTIQIPAVKAFALP 514  
452 TTERPNYESYSHRLSHIGIILLOSERNVPVSTHRSADRNTWTGNRTIOTIEMVAKSELP 511

512	QGT-----TVRGGFGTGGDILRLTNTGGFGPRTVTVNGPLTQRYKIPRYASTVDVDFDFF	566
QY	VERKSPSSVSNANFSRPATGG-----YSRF-----DYVDTLVTTFNQSGVEIIINQLSGY-HL	624
Db	515 AGTYAGGYVTAGPGYTGDDVTPLPYQASL-KIRLT-SAPTMKNTVRRLRYASGGPGPPR	572
QY	567 VSR-GGTVNFRFLRTMNSGDELKYNFVRRAFTPTPTTQIQDIIRTSIOGLSNGEIV	625
Db	625 IVDKVEFPIPIDIQIEKTKCOFEGDICRCGEQVQSLETKEIVNSLFIN	672
QY	626 YIDKIEIIPV-----TATFEAE-----YDLERAQEAVALNFTN	658
Db		

```

KI novel crys gene nignly toxic to Anomala cuprea (Coleoptera:
RT Scarabaeidae)."
RL B1c1. Control 28:191-196(2003).
RL ENML; AB089299; BAC07226.1; -, Genomic_DNA.
DR HSP; Q08117; IJI6.
DR GO: GO:0016787; F:Hydrolase activity; IEA.
DR GO: GO:0005102; F:receptor binding; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR GO: GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SQ SEQUENCE 1144 AA; 128060 MW; 98F93070C49014AB CRC64;

Query Match 21.2%; Score 754; DB 2; Length 1144;
Best Local Similarity 32.7%; Pred. No. 1.4e-45;
Matches 242; Conservative 108; Mismatches 259; Indels 130; Gaps 32

QY 6 SYQNTNEYETLDGSPNNNTNSN--RYPFAXD-----PNIFFPNL 42
DB 2 SPNNQNEYETLDASSSTVSVDNSVRYPLANDQTTLQNMNYKYLRMSEGENPELF----- 57
QY 43 DACQGRPWQDWESVSDIVT---IGTYLIQFLAEPGGIGGIPVIES-IINKLIPSSGQSA 98

```

```
Db 58 ---GNP--ETFISSSTVQTGIGVGVQVGLGALGVPPFAQIASFYFIVQGLWPSVTSVM 111
Qy 99 ALSTCDLVSITRKEVDESVLSDGVADPFGEMTAYQDYLYHLEWLTOKSPKKLADVVK 158
Db 112 EMIMKQVEDLIDQKITDSVRKTALAGLQ--LGDGLDVYQSKLKNLENRNDTRARSVVVT 170
Qy 159 QFOAREDF--TKLAGSLSRQAEILLPTVVOANVHLLLRDLAVKYKKEWGLVCPPLY 217
Db 171 QYIALELDFVAKIPFALSQ--EVLPSVVAQAANLHLLLRDASIFGAEWGFT----- 223
Qy 218 PGSGRTDCNERLAKIKETNYCYGVWYKGLDQIRAGTSAEVWSKFNKFRREMTLAVLD 277
Db 224 PGEIST-PYDQVTFETAGSYCYKWNVTGLDKL--GTNAASWLKYHQFREMTEMLVLD 280
Qy 278 IIAIPPTVDFEYKPLATSVELTREITVPGVY----SGG---NYGWERFFFSNSVEANGT 330
Db 281 LVALLFPNYDTRTYPIETTAQLTREVTDPVFNRETSGGFCRRWSLNSDISFSEVESAVI 340
Qy 331 RPPGLVTLWLAIDYSHSINILQ---YLSGWGTRHYEDFTKGNAGAFQRMST--TSNPP 386
Db 341 RSPHLFDILSIEFYTTAGLPLANNTEYLEYVWVGHSIKYKNTNASSALERNYGTITSNKI 400
Qy 387 RNIIFGNTDIFKIIS---LARYAMQPFVGYISIPRHLVSRAEFFPTTLNTFLYVNSGY 442
Db 401 KYIDLANKDIFQVRLSLGDLANYAQV---YGVF-----YASFTLLDKNTSGSGVGGTY 452
Qy 443 SQ-----TIESVLPGINKOLPPGRTNYSHLSNAACV---QNETS-----RV 481
Db 453 SKPHTTMQVCQNTYNTIDEIP--ENEPLSR-GYSHLSHITSYSFKNASSPARYGNL 508
Qy 482 NVFGWTHSMKDNRIYDPDKITQIPAVKAPALPAGTYAGGVYVAGPYTGDDVVTLFYQ 541
Db 509 PVFANTHSADVNTVYSKDIQIPVKAHTLVSGT-----TVIKGPGFTGNNILKRTSS 563
Qy 542 ASLKIRLTS--APTWNVRLRYASGGPGPRVERWSPSSVSNANFSRATGG---YS 595
Db 564 GPLATYSVSVKSPUSQPRARIRYATNTNRLFV--TISGTRIYSINVNKTMKNGDGLTFN 622
Qy 596 SFDYVDTLVTFNOSGVBIII-----QNLGSHLIVDVEFIPIDIOIEKCTKCFEGDI 650
Db 623 TFD-LATIGTAFSTFNSDSLTVGADSPASGGEVVDKFLIPVN-----ATFEAB- 672
Qy 651 CRCEGVQLETKKEIVNSL 669
Db 673 -----EDLVAKKAVKNL 685
```

## RESULT 14

```
CRIBA BACTE STANDARD; PRT; 1228 AA.
ID POA374; P05517; Q45731;
AC 01-NOV-1988 (Rel. 09, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin
GN CryIIa(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
OS Name=cryIIa; Synonyms=cryA4, cryIIb(a);
OC Bacillus thuringiensis subsp. entomocidus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1436;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects (By similarity).
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus (By similarity).
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
```

CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

DR EMBL; X95704; CAA65003.1; -; Genomic\_DNA.

DR HSSP; P07130; 1DLG.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin\_C.

DR InterPro; IPR005639; endotoxin\_N.

DR Pfam; PF03944; Endotoxin\_C; 1.

DR Pfam; PF00555; Endotoxin\_M; 1.

DR Pfam; PF03945; Endotoxin\_N; 1.

DR Sporulation; Toxin.

QY SEQUENCE 1228 AA; 139622 MW; 3DA2A4DBF59C95C3 CRC64;

## Query Match

Best Local Similarity 21.2%; Score 754; DB 1; Length 1228;

Matches 222; Conservative 121; Mismatches 263; Indels 102; Gaps 29;

```
Qy 11 NEYEILDGSPNNTNMSNRYPPAKDPNIPPI-----NLDACQGRPWQDTWESVDIVTIGY 66
Db 7 NENEIINAVSNHSAQMOLLDPARIEDSLCIABGNMID-----PFVSA-STVQTGINIAGR 60
Qy 67 LIQFLLEPGIGGIPVIFS-IINKLIPSSGQSVAALISICDLVSIIRKEVDESVLSDGVADF 125
Db 61 ILGLVGFPAQGLASFYSLVGLWLP-RGRDQWEIFLEHVEQLINQOITENARNTALARL 119
Qy 126 EGETAYQDYLYHLEWLTOKSPKKLADVVVKQFOAREDEFTKLAGSLSRQAEILL 185
Db 120 QGLGDSFRAYQ-QSLEDWLENRDDARTSVLTVQIALELDFLNPALFAIRNQ-EVPLL 177
Qy 186 PTYQAANVHLLLRDAVKYKKEWGLVCPPL---YPGSGRTDCNERLAKIKETNYCVG 242
Db 178 MYQAANLHLLLRDASLFGSEFGLTSEIQRYV-----ERQVTRDYSYCV 228
Qy 243 WYNGKLDQIRAGTSAEVWSKFNKFRREMTLAVLDLIAIPFYDPEKYPLATSVELTREI 302
Db 229 WYNTGLNLR--GTNAASWVRYNQFRDLTLGLDLVALFPSTYRTYPTINTSAQTREV 286
Qy 303 YTDVPGYSGNNGWERFF-----SPNSVEANGTRGGLVTLWLAIDYSHSINILQGLYS 357
Db 287 YTDATGATGVNMAWMNNNNNAPSFAIEAAAIRSPHLLDFLEQLTIFSGAS-----S 338
Qy 358 GWGGRHYEDFTKGNAGAFQRMSTG-----TTSNPNRIIFGNTDIFKIISLARYA 406
Db 339 RWSNTRHM-TYWRGHTIQSRPIGGGLNTSTHCAATNTSINPVTLRASRDVRYTESYAGVL 397
Qy 407 MQPFVGVYISIPRHLVSRAEF-PPTTLNTFLYEVNSSGYSTIESVLPGI-----NKDLPPS 460
Db 398 LWGI--YLEPIHGVTFRFNTPNQ--ISDRGTANYSQPYES--PGLQKDSLETLPPE 451
Qy 461 RT-----NYSHLSNAACVQNETSRVNVFGWTHSMKKNRIYDPDKITQIPAVKAPALP 514
Db 452 TTERPNYESYSHLSHIGILLOSrvNVVYSWTHRSADRTNTIGPNRIITQIPMKASELP 511
Qy 515 AGTGAGGVVYTAGPGYTGDDVVTLPYQASL-KIRLT-SAPTNNKVNRYRLRYASGGPGPR 572
Db 512 QGT-----TVVRGPGFTGDDILRRNTNTGCGFPIRVTVNGPLTQRYIGFRYASTVDPDF 566
Qy 573 VERWSPSSVSNANFSRATGG-----YSSF---DYVDTLVTFNOSGVBIIIQNLGY-HL 624
Db 567 VSR-GGTTVNNRFLRTNWSGDELKYGNEVRAFTPTFTTQIQDIIRTSIQGLSGNGEV 625
Qy 625 IVDKVEFTPIDIOIEKCTKCFEGVQSLETKEIVNSL 672
Db 626 YIDKIEIIPV-----TATFEA-----YDLERAQAEVNAALFTN 658
```

## RESULT 15

Q93T75\_BACTE

ID Q93T75\_BACTE PRELIMINARY; PRT; 1228 AA.



Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	801.5	22.5	1156	2	S19306	parasporal crystal	
2	756	21.3	1228	2	S00873	parasporal crystal	
3	752.5	21.2	1160	2	I40589	parasporal crystal	
4	716	20.1	719	2	I39815	insecticidal prote	
5	713	20.1	719	2	I39814	insecticidal prote	
6	713	20.1	719	2	S25383	parasporal crystal	
7	710.5	20.0	719	2	I40590	parasporal crystal	
8	682.5	19.2	1138	2	A48944	cryV465 protein -	
9	680	19.1	652	2	I39811	parasporal crystal	
10	664.5	18.7	659	2	S10228	parasporal crystal	
11	664	18.7	934	2	B28838	parasporal crystal	
12	661	18.6	649	1	JH0261	parasporal crystal	
13	647	18.2	1157	1	S42447	parasporal crystal	
14	644	18.1	1174	2	S32649	parasporal crystal	
15	636	17.9	1180	2	A26858	parasporal crystal	
16	635	17.9	1180	2	I39870	parasporal crystal	
17	629.5	17.7	1154	2	S39536	parasporal crystal	
18	625.5	17.6	1176	2	A48970	parasporal crystal	
19	625	17.6	1177	2	A49785	parasporal crystal	
20	623.5	17.5	1178	1	USBSXH	parasporal crystal	
21	620.5	17.4	618	2	S11445	parasporal crystal	
22	620	17.4	652	2	A27323	parasporal crystal	
23	610.5	17.2	1176	2	JC2219	parasporal crystal	
24	606.5	17.1	1176	2	JT0241	parasporal crystal	
25	605.5	17.0	1176	2	A22617	parasporal crystal	
26	605.5	17.0	934	2	S02215	parasporal crystal	
27	604.5	17.0	934	2	A32798	parasporal crystal	
28	604.5	17.0	1160	2	S32647	parasporal crystal	
29	603.5	17.0	655	2	JC7140	protoxin - Bacillu	



172 AGSLSRKAEILLPTVQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLK 230  
177 NGGSLARQAQILLPSFASAFHLLLRDARTGTWNG-----LYNATPPINTQSKLV 231  
231 AKIKEYTNYCVGNKGLDQIRAGTSABVMSKFNKFRREMTLAVLDIAIAPPTDYDFEKY 290  
232 ELIELYTDYCVHYNRGFNELRQRTSATAWLEPHRYRREMTLAVLDIVASFSSLDITNY 291  
291 PLATSVELTRIYTDVGY-----SCGNVWERFP-----SPNSVEANGTRGPGLVVWLQALD 343  
292 PIETDFQLSRVIYTDPIGFVHRSSLRGSEWFSFVNANFSDLE-NAIPNRPSPWFLNNMI 350  
344 IYSHSINLQGLVSG-----WGTTRHYEDFTKNGAF--QRMSGTSSNNPRNIIFGNTDIF 397  
351 ISTGSLTLPVSPSTRARVWYGSR--DRISPANSQFITEISGQHTTATQTLGRN--IF 406  
398 KIISLARYAMQPFVGVYSIPRHLVSRAEPFPTT---LNTFLYE--VNSSGYS---QTIES 448  
407 RVDQAQNLDTTYG-----VNRAVFYHDASEGSRQSVYEGYRTTGTIDNPRVQNT 459  
449 VLPINKDLPSRTNYSRLNSA-----ACVQNETSRVNVFGWTHTSMMKDNRIYDP 500  
460 YLPGENS DI-PTPEDYTHILSTINLTGGLRQVANSRRSSIVMGWTHKSLARNNTINPD 518  
501 KITQIPAVKAFALPAGTYAGGYVTAGPGYTGDDVVTLPYQASLKIRLTSAPTIN--KNYR 558  
519 RITQIPLTKVDTGRGTGSVYN-----DPGFIGALLQRTDHGSLGVLVRVQFPLHLRQQR 573  
559 VRLRYASGGPGPFRVERMSPSSVSNANFSRPAT-----GGYSSPDYDVTLVTFNQ 609  
574 IRVRYAS-----TTNRLSVNGSFGTISQNLPSMTLGEDLRYGSAIRFNTSIRPTASP 629  
610 SGVEIILQ-NLSGYHLIVKVEFIPIDIQIEKCTKQPEGDCRCGEGVQSLETKKEIVNS 668  
630 QDIRLTIEPSFIRQSVVVDRIEFIPVN-----PTR-----EAKEDLEAKKAVAS 674  
669 LF 670  
675 LF 676

RESULT 2  
S00873  
parasporal crystal protein cry8a1 - Bacillus thuringiensis subsp. thuringiensis  
N:Alternate names: parasporal crystal protein cry8a1  
C:Species: Bacillus thuringiensis subsp. thuringiensis  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Oct-2004  
C:Accession: S00873  
R:Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus  
A:Reference number: S00873; MUID:88203216; PMID:3362680  
A:Accession: S00873  
A:Molecule type: DNA  
A:Residues: 1-1228 <BRI>  
A:Cross-references: UNIPROT:P05517; UNIPARC:UPI0000126BDC; EMBL:X06711; NID:g40264; PIDN  
C:Genetics:  
A:Gene: cryA4  
A:Start codon: TTG  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 21.3%; Score 756; DB 2; Length 1228;  
Best Local Similarity 31.4%; Pred. No. 1e-46;  
Matches 222; Conservative 121; Mismatches 263; Indels 102; Gaps 29;  
11 NEYEILDGSPNNWNSRYPFAKDPNIFPI-----NLDACQGPWQWTSVSDIVTGY 66  
7 NENEIINAVNSHAQMDLLPDARIEDSLCIAEGNNID-----PFVSA-STVQTGINIAGR 60  
67 LIQFLERIGGIPVIFS-IINKLIPSSQSVAAALSIDLVSIIRKEVDESVLSDGVADF 125

Db QY 61 ILGLVGVPFAGQASFSYFLVGLWLP-RGRDQWEIHFLEHVEQLINQOITENARNTALRL 119  
QY 126 EGETAYQDYLYLHYLEDMLTDSKNPKLADVVKQFOAREDFTKLLAGSLSRKAEILL 185  
Db QY 120 QGLGDSFRAYQ-QSLEDWLENRDDRARTSRVLTQYIALELDLFLNAPLFAIRNQ-EVPL 177  
QY 186 PTVQANVHLLLRDAVKYKKEWGLVCPPL---YPGSGRTDCNRLKAKIKEYTNYCVG 242  
Db QY 178 MYQAQANLHLLLRDASLFGSEFGLTSQEIORY-----ERQVETRIYSDYCV 228  
QY 243 WYKGLDQIRAGTSABVMSKFNKFRREMTLAVLDIAIAPPTDYDFEKYPLATSVELTREI 302  
Db QY 229 WYNTGLNSLR--GTNAASWVRYNQPRDLTLGLVLDLVALFSPDYTRTPINTSAQLTREV 286  
QY 303 YTDPIVYSGNGVWERFP-----SPNSVEANGTRGPGLVVWLQALDIAIYSHSINLQGLYS 357  
Db QY 287 YTDAGTGVGNVWASNNVNNNAPSFAIAEAAIRSPHLLDLFLBQLTIFSA-----S 338  
QY 358 GGGTTRHYEDFTKNGAFQFMSG-----TTSNNPRNIIFGNTDIFKIISLARYA 406  
Db QY 339 RWSNTRHM-TYWRGHTIQSRPIGGGLNTSTHGAATNTSIMPVTLRFASRDVIRTESVAGVL 397  
QY 407 MQPFVGVYSIPRHLVSRAEF-FPTTLNTFLYEVNSSGYSQTIESTVLPFI-----NKDLPPS 460  
Db QY 398 LWGI--YLEPIHGVPVRFNTPQN--ISDRGTANYSQYES--FGLQLKDSSETELPPE 451  
QY 461 RT-----NYSHRLSNAACVQNETSRVNVFGWTHTSMMKDNRIYDPKITQIPAVKAFALP 514  
Db QY 452 TTPERNYSYSHRLSHIGIILQSRVNVVYWSWTHRSADRTNTIGPNRITQIPMVKASELP 511  
QY 515 ACTGAGGVVYAGPGYTGDDVVTLPYQASL-KIRLT-SAPTNNKRYVRLRYASGGPGPPR 572  
Db QY 512 QET-----TVRGPFTGGDILRRNTNNTGFGPIRVTVNGPLTQRYGRFYASTVDFDFF 566  
QY 573 VERMSPSSVSNANFSRPATGG-----YSSF-----DYDVLTVTFNQSGVEIILQNLGY-HL 624  
Db QY 567 VSR-GGTVNNFRFLRTWNSGDELKYGNFVRAFTPTFTTQIQDIIRTSIQGLSGNGEV 625  
QY 625 IVDKVEFPIDIQIEKCTKQPEGDCRCGEGVQSLETKKEIVNSLFIN 672  
Db QY 626 YIDKIEIIPV-----TATFEAE-----YDLERAQEAVALNFTN 658

## RESULT 3

I40589  
parasporal crystal protein cry8a1 - Bacillus thuringiensis  
N:Alternate names: parasporal crystal protein cryiii  
C:Species: Bacillus thuringiensis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Oct-2004  
C:Accession: I40589  
R:Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano, H.  
Curr. Microbiol. 28, 15-19, 1994  
A:Title: Cloning, heterologous expression, and localization of a novel crystal protein gene  
A:Reference number: I40589; MUID:94100786; PMID:7764305  
A:Accession: I40589  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1160 <RES>  
A:Cross-references: UNIPROT:O45706; UNIPARC:UPI0000126CPE; EMBL:U04366; NID:g532523; PIDN  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 21.2%; Score 752.5; DB 2; Length 1160;  
Best Local Similarity 31.4%; Pred. No. 1.7e-46;  
Matches 233; Conservative 121; Mismatches 251; Indels 137; Gaps 35;  
6 STQNTNEYILDG-SPNN-TNWSNRYPPAKDPNIFPILNDACQGPWQ----- 52  
2 SPNNQNEYIIDLSPTSVSDNSIRYPLAND-----QTNLTQNNMYKDYLRKMTSTNAE 55  
53 -----TWESVSDIVTGYLIQFLLEPGIGGIPV---IFSINKLI-----PSSGQSVAA 99  
56 LSRNPGTFTISAQDAVGTGIDIVSTIIS-GL-GIPVLGEVPSILGSLGLLWPSNNENWQ 113

[illegible]

QY 1 MKNMNSYQNTNEYEYIELDGSPNNTNMSNRYPPAKDPNIPINILDACQGRPWQDTWESVSDI 60  
DB 3 LKNQDKHOSFSSNAKV--KISTDSLKNE-----TDIELQINIHEDCLK---MSEYENVEPF 54  
QY 61 VTIGTYLQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAAALSICD 104  
DB 55 VSAST-----IQTGIGTAGKILGTGVPFAGQVASLYSFLIGELWP-KGNQWEIFMEH 107  
QY 105 LVSIIIRKEVDSVLSDGVADPEG---EMTAYQDYVLYHLEDWLTDKSNPKKLADVVVKQFQ 161  
DB 108 VEEIINQKISTYARNKALTDLKGLDALAVYHD-----SLESWVGNNRNTRAERSVVKSQYI 163  
QY 162 AREEDFTKLLAGSLRQKAEILLPTYYQAAVNHLLLRDAVKYKKEWGLVCPPLYPGSG 221  
DB 164 ALELMFVQKLP-SFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSEI----- 217  
QY 222 RTDCNERLKAKIKEYTNYCVGWYKNGLDQIROAGTSAEYVSKFNKFRREMTLAVLDIAI 281  
DB 218 STFYNRQVE-RAGDYSYHCVKWSYGLNLR--GTNAESWVRYNQFRDMTLMVLVDLVAL 274  
QY 282 PFTYDFEKYPLATSVELTREIYTDVPG-----YSGGNYGWERFFSFSNVEANGTRGPG 334  
DB 275 FPSYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFTSTTYNNNAPSFAIEAAVVRNPH 334  
QY 335 LVTMLOAIDY---SHSINLQGLSGWGGTTHYEDFTKNGAFO---RMSGTTNNPRN 388  
DB 335 LLDLEQVITYISLLSRWSNTQ--YNNMWGG--HKLEFRTIGGTLNISTQGSTNTSINPVT 390  
QY 389 IIFGNTDIFKIIISLA---RYAMQPFVGYISIPHLVSRAEF-----FPTTLNTELYEVNS 439  
DB 391 LPFTSRDYRTESLAGLNLFTQPVNG-----VPRVDFHWKFVTHPIASDNFY--- 439  
QY 440 SGYSOTIESVLPKINGKDLPPSRT-----NYSHLSNAACVQNETSRVNVFGWTHTSMMK 493  
DB 494 DNRIYDPKITQIPAKAFALPAGTGYAGGYVYTAGYTGDDVVTLTPYQASL-KIRLT-SA 551  
QY 499 TWTIEPNSITQIPLVKAFNLSSGAA-----VVRGPGFTGGDILRRNTNTGFDIRVNI 553  
DB 552 PTNKYRVRRLRYASGGPGPFRVERMSPSVSNANFSRATGG-----YSSFDYVDLVTTF 607  
QY 554 PPAQRYRVRIRYASTTDLQFHTS-INGKAINQGNFSATMNRGEDLDYKTFRTVG-FTT 611  
DB 608 N-----QSGVEIIOQL-SGYHLIVDKVEFIPIDIOIEKCTKQFEGDICRCGVQSLETK 662  
DB 612 SFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVTV-----EAYDFEKA 656  
QY 663 KEIVNSLF 670  
DB 657 QEKVTALF 664

## RESULT 6

S25383  
N:Parasporal crystal protein cryIIa1 - Bacillus thuringiensis  
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV  
C:Species: Bacillus thuringiensis  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 05-Oct-2004  
C:Accession: S25383  
R:Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
Mol. Microbiol. 6, 1211-1217, 1992  
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
A:Reference number: S25383; MUID:92269582; PMID:1588820  
A:Accession: S25383  
A:Molecule type: DNA  
A:Residues: 1-719 <TAI>  
A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI000002DB73; EMBL:X62821; NID:g40289; PIDN  
C:Genetics:  
A:Gene: cryV  
A:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 20.1%; Score 713; DB 2; Length 719;  
Best Local Similarity 30.2%; Pred. No. 6.3e-44;  
Matches 220; Conservative 128; Mismatches 256; Indels 124; Gaps 34;  
QY 1 MKNMNSYQNTNEYEYIELDGSPNNTNMSNRYPPAKDPNIPINILDACQGRPWQDTWESVSDI 60  
DB 3 LKNQDKHOSFSSNAKV--KISTDSLKNE-----TDIELQINIHEDCLK---MSEYENVEPF 54  
QY 61 VTIGTYLQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAAALSICD 104  
DB 55 VSAST-----IQTGIGTAGKILGTGVPFAGQVASLYSFLIGELWP-KGNQWEIFMEH 107  
QY 105 LVSIIIRKEVDSVLSDGVADPEG---EMTAYQDYVLYHLEDWLTDKSNPKKLADVVVKQFQ 161  
DB 108 VEEIINQKISTYARNKALTDLKGLDALAVYHD-----SLESWVGNNRNTRAERSVVKSQYI 163  
QY 162 AREEDFTKLLAGSLRQKAEILLPTYYQAAVNHLLLRDAVKYKKEWGLVCPPLYPGSG 221  
DB 164 ALELMFVQKLP-SFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSEI----- 217  
QY 222 RTDCNERLKAKIKEYTNYCVGWYKNGLDQIROAGTSAEYVSKFNKFRREMTLAVLDIAI 281  
DB 218 STFYNRQVE-RAGDYSYHCVKWSYGLNLR--GTNAESWVRYNQFRDMTLMVLVDLVAL 274  
QY 282 PFTYDFEKYPLATSVELTREIYTDVPG-----YSGGNYGWERFFSFSNVEANGTRGPG 334  
DB 275 FPSYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFTSTTYNNNAPSFAIEAAVVRNPH 334  
QY 335 LVTMLOAIDY---SHSINLQGLSGWGGTTHYEDFTKNGAFO---RMSGTTNNPRN 388  
DB 335 LLDLEQVITYISLLSRWSNTQ--YNNMWGG--HKLEFRTIGGTLNISTQGSTNTSINPVT 390  
QY 389 IIFGNTDIFKIIISLA---RYAMQPFVGYISIPHLVSRAEF-----FPTTLNTELYEVNS 439  
DB 391 LPFTSRDYRTESLAGLNLFTQPVNG-----VPRVDFHWKFVTHPIASDNFY--- 439  
QY 440 SGYSOTIESVLPKINGKDLPPSRT-----NYSHLSNAACVQNETSRVNVFGWTHTSMMK 493  
DB 440 PGYA-GIGTQLODSENEIPEATGQPNYESYSHLSHIGLISASHVKALVYSWTHRSADR 498  
QY 494 DNRIYDPKITQIPAKAFALPAGTGYAGGYVYTAGYTGDDVVTLTPYQASL-KIRLT-SA 551  
DB 499 TWTIEPNSITQIPLVKAFNLSSGAA-----VVRGPGFTGGDILRRNTNTGFDIRVNI 553  
QY 552 PTNKYRVRRLRYASGGPGPFRVERMSPSVSNANFSRATGG-----YSSFDYVDLVTTF 607  
DB 554 PPAQRYRVRIRYASTTDLQFHTS-INGKAINQGNFSATMNRGEDLDYKTFRTVG-FTT 611  
QY 608 N-----QSGVEIIOQL-SGYHLIVDKVEFIPIDIOIEKCTKQFEGDICRCGVQSLETK 662  
DB 612 SFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVTV-----EAYDFEKA 656  
QY 663 KEIVNSLF 670  
DB 657 QEKVTALF 664

## RESULT 7

I40590  
C:ryv465 protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Oct-2004  
C:Accession: I40590  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I40590  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>

A;Cross-references: UNIPROT:Q45709; UNIPARC:UPI000003600C; EMBL:U07642; NID:G467234; PID: C;Genetics: cryV465  
A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBI:112093)  
C;Superfamily: Parasporal crystal protein

Query Match 20.0%; Score 710.5; DB 2; Length 719;  
Best Local Similarity 31.0%; Pred. No. 9.6e-44;  
Matches 222; Conservative 120; Mismatches 244; Indels 129; Gaps 33;  
QY 1 MKNMNS--YONTNEYEILDGSPNNTNMSNRYPAKDPNIPPINLDACQGRPWQDTWESVS 58  
DB 34 LKNMNEDEYLRSEHSID-----PPV-----SAS 58  
QY 59 DIWT---IGTYILFLEPGIGGIPVIFS-IINKLIPSSQSVAAALSICDLVSIIRKEVD 114  
DB 59 TIQTGIGAKILGTGVFPAQIASLYSIFLGELWP-KGKSOWEIFMEHVEBELINQKIL 117  
QY 115 ESVLDGVADFEGEMTAYQDYLYHYLEDWLTOKSNPKKLADVVVQFOAREEDFTKLLAGS 174  
DB 118 TYARNKALSDRLGLDALAVYH-ESLESWVENRNTRARSVVKNQYIALELMFVQKLP-S 175  
QY 175 LSRQAEIILLPTVYQAAANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCHERLKAIX 234  
DB 176 FAVSGEEVPLLPYIAQAANHLHLLLRDASIFGKEWGLSASEI-----STFYNRQVE-RTR 229  
QY 235 EYTNVGVWYKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIFPTDYDEKYPLAT 294  
DB 230 DYSDDCHIKWYNTGLNLR--GTNAKSWVYNGFRKDMTLWLDLVALFSDYDLVYPIKT 287  
QY 295 SVELTREIYTPGVYSGGNYG-----W--ERFFSFSNVEANGTRGPGVLTWLOAIIY-- 345  
DB 288 TSQLTREYVTDAGTVHPNQAFASITWYNNAPSFSAIEAAVRSPLHLDLFEKVTIYSL 347  
QY 346 -SHSINLQLGYLSGCGTRHYEDFTKNGAFO---RMSGTTNNPNRIIFGNTPDKIIS 401  
DB 348 LSRWSTNQ--YNNMGG--HRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRES 403  
QY 402 LA--RYAMOPFVGSYIPRHLVSRAEF---RPT---TLNTELYEVNSSGYSQTIESVLPG 452  
DB 404 LAGNLFLTPQVNG-----VPRVDFHWKFTPLPIASDNFY---LGVA-GVGTLQLOD 451  
QY 453 INKDLPPSRT-----NYSRLSNAACVQNETSRVNVFGWTHTSMKKNRIYPKDITQIP 506  
DB 452 SENELPPTGTQPNYESYSHRLSHIGLISASHKALVYSWTHRSADRTNTEPNSITQIP 511  
QY 507 AVKAPALPAGTGYAGGYTAGPGYTGDDVUTLPYQASL-KIRLT-SAPTNKNYRVLRYA 564  
DB 512 LVKAPNLSGAA-----VVRGPGFTGGDILRRTNTGTGDIRVNINPPPAQRYRVRIRYA 566  
QY 565 SGGPFPFRVWRSPSSVSNANFSRATGG-----YSSFDVDTLVTFNOSGVE-----III 616  
DB 567 STTDLQFHTS-INGKAINQGNFSATMNRGEDLDYKTFRTIG-FTTPFSFSDVQSTTIGA 624  
QY 617 QNL-SGYHLIVDKVFIPIDIQIEKCTKQFEGDICRCEGVQSLETKKEIVNSLF 670  
DB 625 WNFSSGNEVIDRIEFVPEVTY-----EAYDFEKAQKVTALP 664

RESULT 8  
A48944  
Parasporal crystal protein cry7Aa1 - Bacillus thuringiensis  
N;Alternate names: parasporal crystal protein cryIIIC  
C;Species: Bacillus thuringiensis  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Oct-2004  
C;Accession: A48944  
R;Lambert, B.; Hofte, H.; Annys, K.; Janssens, S.; Soetaert, P.; Peferoen, M.  
Appl. Environ. Microbiol. 58, 2536-2542, 1992  
A;Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activi  
A;Reference number: A48944; PMID:92384571; PMID:1514800  
A;Contents: BT5137J  
A;Accession: A48944  
A;Status: preliminary  
A;Molecule type: DNA; protein

A;Residues: 1-1138 <1AM>

A;Cross-references: UNIPROT:Q03749; UNIPARC:UPI000002C1E6; GB:M64478; NID:G142760; PID: C;Genetics: cryV465  
A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBI:112093)  
C;Superfamily: Parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 19.2%; Score 682.5; DB 2; Length 1138;  
Best Local Similarity 28.6%; Pred. No. 2.2e-41;  
Matches 208; Conservative 128; Mismatches 262; Indels 129; Gaps 30;  
QY 1 MKNMNSYONTNEYEILDGSPNNTNMSNRYPAK--DPNIFPINLDACQGRPWQDTWE--- 55  
DB 3 LNNLDGYEDSN-----RTLNNSLNYPQTOKALSPSLKNNM-----YQDFLSITE 45  
QY 56 -----SVSDIVTIGTYILFLEPGIGGIPVIP-SIINKLIPSSQSVAAALS 102  
DB 46 REQPEALASNTAINTVSVTGATLSALGVPGASFITNFKIAGLWLPENGK-IWDEBFM 104  
QY 103 CDLVSIIRKEVDESILSDGVADPEGEMTAYQDYLYHYLEDWLTOKSNPKKLADVVVQFOA 162  
DB 105 TEVEALIDQKIEEYVRNKAIAELDLGSLAL-DKYOKALADWLKGQDDPEALSVATEPRI 163  
QY 163 REEDFTKLLAGSLSRQAEIILLPTVYQAAANVHLLLRDAVKYKKEWGLVCPPLYPGSGR 222  
DB 164 IDSLF-EFSMPSFKVTGYEIPLLTVYQAANHLHLLLRDSTLYGDKWG-----FTQNNI 216  
QY 223 TDCNERLKAKIEYTNVGVWYKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIF 282  
DB 217 EENYNRQKRIRSEYDHCTKWYNSGLSRLN--GSTYEQWINYNFRREMILMALDOLVAVF 274  
QY 283 PTYDFPKYPLATSVELTREIYTPGVYSGGNYGWERFFSFSNVEANGTRGPGVLTWLOAI 342  
DB 275 PHDPRYSMEVSTQLTREYVTPVLSISNP--DIGPFSQMENTAIRTPHLVDYLDL 332  
QY 343 DIY-----SHSINLQLGYLSGCGTRHYEDFTKG-----NGAFQMSGTTNNPNRN 388  
DB 333 YIYTSKYKAFSHEIQPDLFWSA-----HKVSFKSEOSNLYTTGTYGKTSYISSGAYS 387  
QY 389 IIFGNTDIPKISLARYAMOPFVGSYIPRHLVSRAEFPPTLTNTFLYEVNSSGYSQTIES 448  
DB 388 --FHGNDIYRTLAAPSVMVVPYT---QNYGVGEVFEY--GVKGHVYRGDNKYDLTVDS 439  
QY 449 V--LPGINKDLPPSRNYSRHLSSNAACVQNET-----SRVNVFGWTHTSMKKNRIYDPK 501  
DB 440 IDQLP---PDGEPHKEKYTHRLCHATAIFKSTPDYDNATIPISFWTHRSABEYRNPKN 496  
QY 502 ITQIPAVKAPALPAGTGYAGGYTAGPGYTGDDVUTLPYQASLKIRLTSAPTKNYR 558  
DB 497 ITKIPAVKMYKLLDDPS-----TVVKGPGFTGGDLVKGSGTYGIDIKATVNS-PLSQYR 550  
QY 559 VRLRYASGGPGPPRV-----ERWSPSSVSNANFSRATGGYSSFDYVDTLVT-TFNQ 609  
DB 551 VVRVYATNVSQGFNVYINDKITLQTKFQNTVETIGEGKDLT--YGSFGYIEYSTTIQFPD 608  
QY 610 SGVEII-----TONLSGYHLIVDKVFIPIDIQ-IEKCTKQFEGDICRCEGVQSLETKK 663  
DB 609 EHPKITLHLSDLSSNSSFY--VDSIEFIPVDVNYAEK-----EKLEKAQ 650  
QY 664 EIVNSLF 670  
DB 651 KAVNTLP 657

RESULT 9  
I39811  
Parasporal crystal protein cry3Bb1 - Bacillus thuringiensis  
N;Alternate names: parasporal crystal protein cryIIIB2  
C;Species: Bacillus thuringiensis  
C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Oct-2004  
C;Accession: I39811  
R;Donovan, W.P.; Rupan, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burke, M.C.; Johnson, T.  
Appl. Environ. Microbiol. 58, 3921-3927, 1992  
A;Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal cry

A;Reference number: I39811; MUID:931119147; PMID:1476436  
A;Accession: I39811  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-652 <RES>  
A;Cross-references: UNIPROT:Q06117; UNIPARC:UPI0000126C14; GB:M89794; NID:g142729; PIDN:  
C;Genetics:  
A;Gene: cryIIIB2  
C;Superfamily: Parasporal crystal protein

Query Match 19.1%; Score 680; DB 2; Length 652;  
Best Local Similarity 29.5%; Pred. No. 1.4e-41;  
Matches 209; Conservative 125; Mismatches 233; Indels 142; Gaps 33;

Qy 9 NTNEYELDGSPPN---TNNSNRYPFKADNPFIINLDACQG-RPMQDTW-----ESVS 58  
Db :  
5 NRSEHDITKVTPNSELOTN-HNQYPLADNPNSTLEELNYKEFLRMWTSSTEVLNDSTVK 63  
Qy 59 DIVTIGHYLQLFLLPEGIGIP-----VFISIINKLIPISSGOSVAALISCDLVSIIRK 111  
Db :  
64 DAVGTGISVVGQIL--GVWGVPFAGALTSPYQSFPLNTIWPSDADPWKAF-MAQVEVLIDK 120  
Qy 112 EVDESVLSDGVADEGEWTAYQDYLYHLEDMLTDKSNP-----KKLADVVKQFOAREED 166  
Db :  
121 KIEEYAKSKAAELQGLQNFP--YVNALNSW---KTPLSLRSKRQSDRIELFSQAES 176  
Qy 167 FTKLLAGLSRQKAEIILLPTTYQAAHVHLLLRLDAVKYKKEWGLVCPLYPGSGRDCN 226  
Db :  
177 HFRNSMPFAVSKFEVLFLPTYAQAAANTHLILLKDAQVGEEWG-----YSSDEVAFY 230  
Qy 227 ERKAKIKETVNYCVGWYNKGLDQIROAGTSAEVWSKFNFRRBMTLAVLIDIATPYTD 286  
Db :  
231 HRQLKLTQQVTDHCVNVVYVGLNGLR--GSTYDAWKVFNFRREMTLTVDLIVLPFYD 288  
Qy 287 FEKYPLATSVELIREIYTDPVGYSGGNYGWERPFSNSVE-----ANGTRGPGLV 337  
Db :  
289 IRLYSKGVKTELTRDIITFDPI-----FSLNTLOEYGFPLSINIENSRKPHLFD 336  
Qy 338 WLQAIITYSHSINLQYG----LSMGGRTHYEDFTKGNGAFORMS----GTTSNRP-R 387  
Db :  
337 YLOGIEHT--RLQPGYFGKDSFNYHG--NYVETPSIGSSKITITSPPYGDKSTEPVQ 391  
Qy 388 NIIFGNTDIPKIISLAYAMQP-----FVGYSIPRHLSRAEFF-----PTTLINTFLYE 436  
Db :  
392 KLSFDGQKWRTIANTDVAAPNGKVYL-----VTKVDFOYDDQKNETSQTYYDSK 444  
Qy 437 VNSSGYQTTIESVLPGINKOLPPSRTH-----YSHRLSNAAC--VQNETSRVVNVFWTH 488  
Db :  
445 RN-NGHVSAQDSI-----DQLPPTTDEPLEKAYSHQLNYAECEFLMQDRREGTIPFFTW 498  
Qy 489 TSMKKDNRIYPDKITOIPAVKAFALPAGTGAGGYVTAAGCYTGCDVVTLIPYQ----ASL 544  
Db :  
499 RSVDFWTIDAELITQIPVVKAYALS GAS-----IIEGPGFTGNNLLFLKESNSIAKF 553  
Qy 545 KIRLTSAPTNKNYVRILRYAGSGPGPRFRVERSWSPSSVSNANF-----SRPATCGYS 595  
Db :  
554 KVTLNSAALLQRVVRIRYASTNLRLFVN-----SNNDFLVIYINKMKDDDLTYQ 607  
Qy 596 SFDYVDLTVTTFNOSGV-----EIII---QNLSGHYLIVDKVEFIPIDI 636  
Db :  
608 TFD-----LATTNMNGFSGDKNELIIGAESFVSNKEIYIDKIEFIPVOL 652

RESULT 10  
S10228  
parasporal crystal protein cry3Ba1 - *Bacillus thuringiensis* (fragment)  
N:Alternate names: coleopteran-active parasporal crystal protein; delta-endotoxin  
C:Species: *Bacillus thuringiensis*  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 05-Oct-2004  
C:Accession: S10228  
F:Stick, A.; Gaertner, F.; Wong, A.  
Nucleic Acids Res. 18, 1305, 1990  
A:Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of *Ba*

[illegible]

RESULT 11

B29838  
parasporal crystal protein - *Bacillus thuringiensis* subsp. *israelensis* (fragment)  
C:Species: *Bacillus thuringiensis* subsp. *israelensis*  
C:Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 05-Oct-2004  
C:Accession: B29838  
C:Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Wall  
J. *Bacteriol.* 166, 801-811, 1986  
A:Title: Structural similarity between the Lepidoptera- and Diptera-specific i

A:Reference number: A94672; MUID:86223796; PMID:3011746

A:Accession: B29838

A:Molecule type: DNA

A:Residues: 1-934 <THO>

A:Cross-references: UNIPROT:P09662; UNIPARC:UPI00001781A0; GB:M12662; NID:g143228

Query Match 18.7%; Score 664; DB 2; Length 934;

Best Local Similarity 30.5%; Pred. No. 3.6e-40;

Matches 228; Conservative 96; Mismatches 273; Indels 150; Gaps 34;

QY 4 MNSYONTNEVEILLDGSNNNTNNSN---RYPPAKDPNIFPIN-----LDACQGRW--- 50

DB 1 MNPYQNKNEYIFNAPNSGFSKSNYSRYPLANKPN-QPLKNTNYKDWLNVCODQOYGN 59

QY 51 -----QDTWESVS-DIVTIGTYILQFLLEPGIGIPVIFSII---NKLIPSSGQSVAA 99

DB 60 NAGNFASSETIVGVSAGIIVGTML-----GAPAPVLAAGIISFGTLLPIFWGSDP 112

QY 100 LSIC-DLVSIIRKEVDE-----SVLSDGVADPEGEMTAYQDYLYHLEDM---LTDKSNP 150

DB 113 ANVQDOLLNIGRPQIEIDKNIINVLTSIVTPIKNLQDKYQEFF---DKWEPARTHANA 168

QY 151 KKLADVQKQFQAREEDFTKLAGLSRQKAEILLPTTYQAAHVHLLLRDAVKYKKGW 210

DB 169 KAVHDL---FTTLEPIIDKDLMLKNNASYRIPTLPAYAQIATWHLNLLKHAATYTNIW- 224

QY 211 LVCPPLYPGSGRTD-CNERLAKIKEYTNYCVGWYKGLDQIROAGTSAEYWSKENKER 268

DB 225 LQNGINSTFTSNYYQYLKRRKIQEYDYCIQTYNAGLTWIR-TNTNA-TWNMYNTYR 282

QY 269 REMTLAVLDIIAIFPTYPEKYPLATSVELTREIYDVPVSGYGNWGRFFSFNSVEAN 328

DB 283 LEWTLVLVDLIAFPNDPEKPIGVKSELIREVY-----NVNSTFTTITILENG 334

QY 329 GTRGPGLVTLWQAIDIIYSHSINLQGLYSGWGTTRHYEDFTKNGAF-----QRMSCGTTN 384

DB 335 LTRNPTLFTWINGRFPY-----TRNSRDILDYDIFSTFGNQMAFTHTN 378

QY 385 NPNRIIFG-----NTDIFKIISLARYAMQPFVGSIPRH-----LVSRAEFFPTTLNT 432

DB 379 DDRTNIWAGVHGNIIISQDTSKVPFP--YRNKPIDKVEIVRHREYSIDIYEMIFFSNSSEV 436

QY 433 FLYEVNSSGYSTIESVLPGLNKDLPSPRT---NYSHRLSNAA-----CVQNETSRVN 482

DB 437 FRYSNS-----TIENNYKRTDSYMLPKQTKWNEEYCHTSLYIKTDNYIFSVVRERRV- 490

QY 483 VFGWHTSMKKDNRIYPDKITQIPAVKAFALPAGTGYAGGYTAGPGYTGDDVVTLPYQA 542

DB 491 AFSWHTTSVDFQNTIDLDNIQIHALKALKVSSDS-----KIVKPGHTGGDLVILKDSM 545

QY 543 SLKIRLTSAPTWNTVRRLRYASGGP-----GPFVRWSPSSSVSNANFSRATG- 592

DB 546 DFRVFLK-NVSRQVRIRYATNAPKTVFLTGIDTISVELPSTTSRQPN-----ATDL 600

QY 593 GYSSFDYVDLVTTFNQSG--GVEIILQNLG-----YHLIVDKVEFIPIDQIEKTKCQ 645

DB 601 TVADFGYVTFPRVFNKTFEGEDTLMTLYGTPNHSNIYIDKIEFIPITQSVLDYTE-- 658

QY 646 FEGDICRCBGVQSLETKKEIVNSLFIN 672

DB 659 -----KQNIETQKIVNDLFWN 675

RESULT 12

JH0261

N:Alternative names: parasporal crystal protein cry3Ca1 - Bacillus thuringiensis subsp. kurstaki (strain Bt11

C:Species: Bacillus thuringiensis subsp. kurstaki

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 05-Oct-2004

C:Accession: JH0261; S18944

R:Lambert, B.; Theunis, W.; Aguda, R.; Van Audenhove, K.; Decock, C.; Janssens, S.; Seuri

Gene 110, 131-132, 1992

A:Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crystal

A:Reference number: JH0261; MUID:92184108; PMID:1544571

A:Accession: JH0261

A:Molecule type: DNA

A:Residues: 1-649 <LAM>

A:Cross-references: UNIPROT:Q45744; UNIPARC:UPI0000126C15; EMBL:X59797; NID:g40287; PID

C:Genetics:

A:Gene: cryIIID

C:Superfamily: Parasporal crystal protein

Query Match 18.6%; Score 661; DB 1; Length 649;

Best Local Similarity 30.3%; Pred. No. 3.4e-40;

Matches 216; Conservative 108; Mismatches 234; Indels 156; Gaps 35;

QY 9 NTEYBILDSPPN---TNMSNRYPPAKDPNIFPINLACQGRPWQDTWESV---SDIV 61

DB 5 NRSEHTIKATENNEVSNHQAQPLADTPTLEELNYKEFLRRTDNNVEALDSSTTKDAI 64

QY 62 TIGTYILQFLLEPGIGIP-----VIF--SIINKLIPSSGQSVAAALSICDLVSIIRKEDV 114

DB 65 QKGISIIGDLL--GVGFPYGGALVSPYTNLLNTWIP--GEDPLKAFMQQVEALIDOKIA 120

QY 115 ESVLSGCVADPEGEMTAYQDYLYHLEDMTLTKSNPKKLADVVVKQFOARE-----EDFTK 169

DB 121 DYAKDKATAELOGLKNVFKD--YVSALDSW--DKT-PLTLRDGRSQGRIRLELFSQAESHFR 176

QY 170 LLAGSLSRQKAEILLPTTYQAAHVHLLLRDAVKYKKEGLVCPPLYPGSGRTDCNERL 229

DB 177 RMPSPFAVSGYELFPLPTTAQAAANTHLLLDKQAIYGTDWG-----YSTDDLNEFHTKQ 230

QY 230 KAKIKEYTNYCVGWYKNGLDQIROAGTSAEYWSKFNKFRREMTLAVLDIIAIFPTYDPEK 289

DB 231 KDLTIEYTHCAKWKYKAGLDKLR--GSTYEWKFNRYRREMTLVLJDLTLFLPLYDVRT 288

QY 290 YPLATSVELTREIYDTPV-----GYSGYGNWGRFFSFNSVEANTRGGLVTLWQA 342

DB 289 YTKGVKTELTRDVLTPIVAVNNMGVY-----TTFSNIE-NYIRKPHLFDYLHAI 338

QY 343 DIYSHSINLQGLYSGWGTTRHYEDFTKNGAFQFMS-----GTTSN-NPNRI 389

DB 339 QFHS-----RLQPGYF-----GTDSEF-NYWSGNYVSTRSSIGSEIIRSPFYGNKSLDQVNL 390

QY 390 IFGNTDIFKIISLARYAMQPFVGSIPRHLSRAEFPPTLTNTFLYEVNSSGY----- 442

DB 391 EFNKEGVKRAVANGNLAVWP-VGTG-----GTXHSGVTYKQSFQYNDKRDVEV 437

QY 443 -SQTIES-----VLPGINKDLPSPRTN-----YSHRLSNAAAC--VQNETSRVNVFGW 486

DB 438 RTQTYDSKRNVGSGIVFDSIDQ-LPPTTDBSEKAYSHQLNYYVRCFLQGGRIIPVFTW 496

QY 487 THTSMMKDNRIYPDKITQIPAVKAFALPAGTGYAGGYTAGPGYTGDDVVTLPYQASIKI 546

DB 497 THKSVDFTYNTLDSSEKITQIPFVKAFILVNST-----VWAGPGFTGGDIICKTNGSGTLT 551

QY 547 RLTSAPT--NKNYRVLRYASGPGPFVRWSPSSSVSNANFSRATGGSV-SFDYVD- 601

DB 552 YTPAPDLTYSTYKIRIYASTSQVRFGID-----LGSYTHSISIFPDK 595

QY 602 -----TLV-TTFNQSGV---EIIQNL-----SGYHLIVDKVEFIPID 635

DB 596 TMDKGNLTLYNSFNLSVSRPIEISGKNKIGVSGVGGIGSGDEVYIDKIEFIPMD 649

RESULT 13

S49247

N:Alternative names: parasporal crystal protein cry9Ca1 [validated] - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 05-Oct-2004

C:Accession: A59350; S49247

R:Lambert, B.; Buyasse, L.; Decock, C.; Janssens, S.; Plens, C.; Saey, B.; Seurinck, J.;

Appl. Environ. Microbiol. 62, 80-86, 1996

A:Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity aga

A:Reference number: A59350; MUID:96141404; PMID:8572715

A:Accession: A59350  
A:Molecule type: DNA  
A:Residues: 1-1157 <LAM>  
A:Cross-references: UNIPROT:Q45733; UNIPARC:UPI000002F5A5; EMBL:Z37527; NID:G547554; PID:1-1157 <LAM>  
A:Experimental source: serovar colworthi  
C:Comment: This parasporal crystal protein, active against corn borer and other insects,  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 18.2%; Score 647; DB 1; Length 1157;  
Best Local Similarity 27.3%; Pred. No. 8.8e-39;  
Matches 198; Conservative 127; Mismatches 287; Indels 112; Gaps 25;  
QY 9 NNEVEILD---GSPNNMNSNPFYPAKDNIPINLDACQRPWQDTWESVSDIVTIG 64  
DB 5 NQNEYIIDAHPGCGPDDV---RYPLASDPNA-----ALQNMNYKQVLQMTDSDYT-D 55  
QY 65 TYLIQFLLEPGIGIPVIFSIINKL-----IPSSQGSVAALSIC-----103  
DB 56 SYVNPISLSISGRDAVQTALTVVGRILGALGVFPFGQIVSFYQFLNLTLPVNDTALWEAF 115  
QY 104 --DLVSIIRKVESVLSGVDADFGEMTAYODYLHYLEDWLTOKSNPKKLADVVKQFQ 161  
DB 116 MRQVEELVQQTTEFARNQALRQLGLGDSF-NVYQRSQNLQNLADNRNLSVVRQAFI 174  
QY 162 ABEEDFTKLAGSLRQKAEIILLPTTYQAAVNHVHLLLRDAVKYKEWGLVCPPLYPGSG 221  
DB 175 ALDLDFVNAIP-LFAVNGQGVPELLSVYQAQVNLHLLLLKDALSLFGEGWGT-----QGBI 228  
QY 222 RTDCNERLKAKIKEYTNYCVGWYKGLDQIRQAGTSAEVMKFNKPRRMTLAVLDIAI 281  
DB 229 STYIDRQLELTA-K-TNYCETWYNTGLDLR--GNTESWLYHQFRRENTLVLDVAL 285  
QY 282 PFTYDFEYPLATSVELTREIYTPVGYSG-----GNYGWERPFSSFNSEANGTRPG 334  
DB 286 PFYDVRLYPTGSNPQLTREVTDPVFNPPANVGLCRRWGTPNYNTESELENAFIRPPH 345  
QY 335 LVMTLQADIIYSHSINLQYLSGCGTRHYEDFTKNGCAFQRMGTTNNPRNIFGNT 394  
DB 346 LPDRLNLSITISNRPFPVSSNFMVDSGHTLRSLYLNDSAVQDSYGLITTTTRATINPGVD 405  
QY 395 DIFKIISLARYAMQFPVGYSIPIRLVSRAEFFPTTLNTPLEYVNSGYSQTTESVLPGLN 454  
DB 406 GNTRESTAVDRSALIGI-----YGVNRASFVPGGLNGTTTPANGGCRDLDT-----N 456  
QY 455 KDLPPSRNTYS--HRLSNAACVQNETSR-----VNVFGWTHTSMKKNRIYDPKIT 503  
DB 457 DELPDESGSTHRLSHVTFPFSQINQAGSIANAGSVPTVYVTRDVLNNTIIPNRI 516  
QY 504 QIPAVKAFALPAGTAGYAGGYTAGGYTGGDVVTLPIYQASL-KIRLT-SAPTNKNYRVL 561  
DB 517 QLPLVKASAPVSGT-----TLKGPQFTGGILRRTNGTFTGLRVTVNSPLTQQYRLRV 571  
QY 562 RVASGCGPFRVERMSPSSVSNANFSRATGG-----YSSPDYVDTLVT-----TFNQS 610  
DB 572 RFAGTGNFSIRVL-RGVSGIDVRLGTSWNRGOELTYESFFTRFETFTGFPNPPFTFOA 630  
QY 611 GVEIITQNLGSY-----HLIVDKVEFIPIDIIQIEKCTKQFEGDICRCEGVQSLETKEIV 666  
DB 631 -QELLTVNAEGVSTGGEYIDRIEIVPVN-----PAREAEEDLEAKKAV 674  
QY 667 NSLF 670  
DB 675 ASLF 678

RESULT 14  
S32649  
parasporal crystal protein cryIa3 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Oct-2004  
C:Accession: S32649  
R.Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645  
A:Accession: S32649  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <LAM>  
A:Cross-references: UNIPROT:Q45749; UNIPARC:UPI00000BF0F3; EMBL:Z22512; NID:G295865; PID:1-1174 <LAM>  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 18.1%; Score 644; DB 2; Length 1174;  
Best Local Similarity 29.2%; Pred. No. 1.5e-38;  
Matches 202; Conservative 115; Mismatches 255; Indels 120; Gaps 26;  
QY 24 NMSNR---YPPAKDNIPINLDACQRPWQDTWESVSDIVTIGTYLIQFLLEPGIGIP 80  
DB 4 NQNOCVPVNCUSNPEVEILSEERSTGRPLD-----ISLSLTRFLLESEFPGVG 53  
QY 81 VIFSIIINKLIPSSGOSVAALSICDLVSIIRKVESVLSGVDADFGEMTAYODYLHYL 140  
DB 54 VAFGLFDLWGTTFITSEWSLFILOEQLEQRIETLERNRAITTLRGLADSY-EVYLEAL 112  
QY 141 EDWLTDKSNPKKLADVVKQFQAREEDFTKLAGSLRQKAEIILLPTTYQAAVNHVHLLLR 200  
DB 113 REWEENPNNAQLREDVRIRF-ANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLR 171  
QY 201 DAVYKKEWGLVCPPLYPGSGRTDCNERLKAKIKEYTNYCVGWYKGLDQIRQAGTSAEV 260  
DB 172 DAVSFGQCGWGLDIATV-----NNHYRLNLIHRYTEHCLDTYNOGLENLR-GTNTRQ 223  
QY 261 WSKENKFEREMTLAVLDIIAIPTYDFEYPLATSVELTREIYV-----DPVGYSGNY 314  
DB 224 WSKFNQFRRELTVLVDIIVALFPNDARAYPQTSSQLTREIYTSVIEDSPVSAKIPN- 282  
QY 315 QWERFFSFEVSEANGTRGPGVLTWLOAIDYSHSINLQYLSGCGTRHYEDFTKNGA 374  
DB 283 -----GFNRAEF-GVRPPLHMDFMNSLFTAETVRSQ---TWGSG--HLVS----- 322  
QY 375 FORMSGTTSNNPRNI-IFGNTDIFKIISLARYAMQFPV-----GYSIPRHLVS- 421  
DB 323 ----SRNTAGNPNFPIYIGIFNPGGAIWIADEPRPFYRTLSDPVFVRGFGFNPHVYGL 378  
QY 422 RAEPFPTTLNTPLEYVNSGYSQTTESVLPGLNPKDLPPSRNTYSHRLSNAACVQ----- 475  
DB 379 RGVAFOQTNTNTRTFERNSGTIDSLDEIIPQDNGAP--WNDYSHVNLNHTVFRVGEIA 436  
QY 476 -NETSRVNVFGWTHTSMKKNRIYDPKITQIPAVKAFALPAGTAGYAGGYTAGGYTGGD 534  
DB 437 GSDSWRAPMFWSTHRSADRTNIINPNIIQIPAVKAHL-----HSGSTVVRGFGFTGGD 491  
QY 535 VVTLPYQ---ASLKIRLTSAPTNKNYRVLRYASGCGPFRVERMSPSSVSNANFSR- 589  
DB 492 LLRRNTNGTFADIRVNIT-GPLSQRYRVRIRVASTDLQF-FTRINGTSVNOGNFQRTMN 549  
QY 590 -----ATGGVSS-PDYVDTLVTTFNQSGVEIILQNLSGYHLIVDKVEIPIDIIQI 638  
DB 550 RGNLESNGNFRTAGSTPFSFNSA-----QSTFTLTGQAFSNOEYVIDRIEFVPAEVT 603  
QY 639 ECKTKQFEGDICRCEGVQSLETKEIVNSLF 670  
DB 604 EA-----ESD-----LERAQKAVNALF 620

RESULT 15  
A26858  
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N:Alternate names: parasporal crystal protein cryIVA  
C:Species: Bacillus thuringiensis subsp. israelensis  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 05-Oct-2004  
C:Accession: A26858; S48691  
R.Ward, E.S.; Ellar, D.J.  
Nucleic Acids Res. 15, 7195, 1987  
A:Title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding

A:Reference number: A26858; MUID:88015571; PMID:2821500  
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A:Note: the authors translated the codon GCA for residue 308 as Thr  
R:Nishimoto, T.; Yoshisue, H.; Ihara, K.; Sakai, H.; Komano, T.  
FEBS Lett. 348, 249-254, 1994  
A:Title: Functional analysis of block 5, one of the highly conserved amino acid sequence  
A:Reference number: S48691; MUID:94307434; PMID:7913448  
A:Accession: S48691  
A:Molecule type: DNA  
A:Residues: 667-676 <NIS>  
A:Cross-references: UNIPARC:UPI000017819A  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 17.9%; Score 636; DB 2; Length 1180;  
Best Local Similarity 29.1%; Pred. NO. 5.8e-38;  
Matches 219; Conservative 112; Mismatches 288; Indels 134; Gaps 34;

QY	4	MNSYQNTNEYETLDGSPNNTNMSN---RYPFAKDPN--IFPIN-----LDACQ-----GRP 49
Db	1	MNPYQNKNEYETLNASQKLNISNNTRYPIENSFKLLQSTNYKDWLNMCQNOQOYCGD 60
QY	50	WQ---DTWESVSDIVTIGTYLIQFLLEPGIGGIPVF-SIINKLIPSSGQS-VAALSICD 104
Db	61	FEFTIDSGELSAITVVGTVLTGFGFTPLGLALIGFTGLIPVLPFAQDSNTWSDFITQ 120
QY	105	LVSIIKKEVDESVLSDGVADPEGEMTAYQDYVLYHLEWLTDKSNPKKLADVVVKQFARE 164
Db	121	TGNIKKKEIASTYISNANKILNRSFNVISTYHNH-LKTW-ENNPNPQNTQDVRTQIQLVH 178
QY	165	EDFTKL---LAGSLRQKAE-----ILLPTVYQAAVNHLLLRDAVKY-----KEWG 210
Db	179	YHFQVPIPELVNSCPPNPSDCDYINLVLSYQAQAAHLTVLNOAVKFEAYLKNNRQPD 238
QY	211	LVCPLYPGSGRTDCNERLKAKIKVNTYCVGMNKGDLDIR--QAGTSAEV-WSKENK 266
Db	239	Y-----LEPLTAIDYYPVLTAKAIEDYTNVCVTKYKGLNLIKTPTDSNLDGNINNTYNT 294
QY	267	PREMTLAVLDIAIFPTDYDEKYPLATSVELTREIYTDVPVGYSGNYGWERFFSFNSVE 326
Db	295	YRTKMTAVLDVVALFPNVGVGKYPGVQSELTREIY-QVLNFEESPY---KYDFQYQE 350
QY	327	ANGTRGPGLVTLQALDIYSHSINIQLGYLSGCGGTRHYEDPTKNGAPQRMSTSN-N 385
Db	351	DSLTRRPHLFTWLDLSLNFYEKAQTTPNNFF-----TSHYMF-----HYTLDNIS 395
QY	386	PRNIIFGN---TDIEKIISLAR--YAMQPFV-----GYSIPRLVSRAEFFPTTLNTFLY 435
Db	396	QKSSVFGNHNVTDKLSLGLATNIYIFLLNVISLDKNLYNDYNNISKMDFFITNGTRLLE 455
QY	436	EVNSSGYSQTIESVLPFGI-----NKDLPGRNTYSHRLS---NAAVCVQNETS 479
Db	456	KELTAGSGQITVDVKNKIFGLPLKRENOGNPTLFFTYDNYSHILSPKLSLSIPATYKT 515
QY	480	RNVVFGWTHSMKKDNRIYDPKIQIOPAVKAPALPAGTGYAGGYTAGPGYTGDDVTLTP 539
Db	516	QVYTFAMTHSSVDPKNTIYTHLTQIPAVKANSL--GT---ASKVVQPGHGTGGDLI--D 568
QY	540	YQASLKIRLTAPTNTKNTYRVLRYASGGPFR-VERWSPSSVSNANFS-RPATCG----- 593
Db	569	FKDHFKITCQHSNFOQSYFIRIRYASGSANTRAVINLSIPGVAELGMALNPTFSGTDYT 628
QY	594	---YSSFDYVD-----TLVTFNOSGVEIIQNLSGYHLIVDKVEFIPIDIOIE 639
Db	629	NLKYKDFQYLFESNEVKFAPNQNISLVNFRSDV-----YNTTVLIDIKIEFLPTRSIR 682
QY	640	KCTKQPEGDIICRCBGVQSLETKKEIVNSLFIN 672
Db	683	EDRE-----KQKLETVQOIINTFYAN 703

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